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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 24, 2004, 16:13:03 ; Search time 673 Seconds
(without alignments)
3494.414 Million cell updates/sec

Title: US-10-019-341-3

Perfect score: 2385

Sequence: 1 ADOQRDFIDIESKALRTPE.....GRAPAVFKCHDKSLNKSG 448

Scoring table:

BLOSUM62 Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-Q=/cgn2.1/USPTO.spool/US10019341/runat.22102004.120137.1598/app.query.fasta.1.647
-DB=N Geneseq 23Sep04 -QNT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0
-LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blom62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10019341 @CGN 1.1.470 @runat.22102004.120137.1598 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N_Geneseq 23Sep04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2385	100.0	3549	2	AAV41319
2	2385	100.0	3549	2	AAV41319 Human lip
3	2385	100.0	3549	6	AAZ32183 Human lip
4	2385	100.0	3549	6	ABL66907 Lung canc
5	2385	100.0	3549	6	ABT10903 Human bre
6	2385	100.0	3549	6	ABT13006 Human lip
				12	ADM41259 Human lip

7	2385	100.0	4314	12	ADQ23742
8	2378	99.7	3635	9	ACH03823
9	2372	99.5	4075	10	ADB47407
10	2235.5	93.7	3617	10	ADB58085
11	1996	83.7	1584	12	ADF28939
12	1696	71.1	2939	2	AAZ33576
13	1632.5	68.4	2933	2	AAZ33576
14	1161	48.7	1503	6	ABL91801
15	1161	48.7	1755	2	AAZ33605
16	1161	48.7	1755	2	AAZ33605
17	1161	48.7	2565	3	AAV41622
18	1161	48.7	2565	3	AAV41622
19	1161	48.7	3927	8	ACF34500
20	1161	48.7	3927	10	ADE38384
21	1161	48.7	3927	10	ABX08853
22	1161	48.7	3927	12	ADJ25517
23	1161	48.7	3927	12	ADP66749
24	1158	48.6	1839	2	AAZ33605
25	1158	48.6	1839	2	AAZ33605
26	1157	48.5	3610	12	ADP66756
27	1038	43.5	1603	6	ABT13009
28	1038	43.5	1603	6	ABT13009
29	1036	43.4	1553	10	ADC59370
30	1019.5	42.7	1639	10	ADB57969
31	1014.5	42.5	1605	6	ABK63642
32	1014.5	42.5	1605	6	ABK63642
33	962	40.3	1323	10	ADE47727
34	962	40.3	1323	10	ADE47727
35	928	38.9	1035	2	AAV41621
36	928	38.9	1035	2	AAV41621
37	928	38.9	1065	3	AAV41621
38	928	38.9	1065	3	AAV41621
39	928	38.9	1382	2	AAV41620
40	928	38.9	1382	2	AAV41620
41	928	38.9	1509	2	AAZ34041
42	928	38.9	1510	3	AAZ34041
43	928	38.9	1510	3	AAZ34041
44	928	38.9	1510	5	AAZ34041
45	928	38.9	1510	5	AAZ34041

ALIGNMENTS

RESULT 1

AAV41319	AAV41319 standard; DNA; 3549 BP.
ID	AAV41319 standard; DNA; 3549 BP.
XX	
AC	AAV41319;
XX	
DT	09-NOV-1998 (first entry)
XX	
DE	Human lipoprotein lipase gene.
XX	
KW	Lipoprotein lipase; LPL gene; hypertension; exercise; human;
KW	genetic marker; ss.
XX	
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
FT	175..1602
FT	/*tag= a
FT	sig_peptide
FT	175..255
FT	/*tag= b
FT	mat_peptide
FT	256..1599
FT	/*tag= c
XX	
PN	WO9831835-A1.
XX	
PD	23-JUL-1998.
XX	
PF	22-DEC-1997; 97WO-US022974.
XX	
PR	16-JAN-1997; 97US-0035382P.

PR 27-MAY-1997; 97US-0048309P.
 XX (UYMA-) UNIV MARYLAND BALTIMORE.
 PA (UYPI-) UNIV PITTSBURGH.
 XX Hagberg JM, Ferrell RE;
 XX MPI; 1998-414128/35.
 DR P-PSDB; AAM68154.
 XX
 XX Analysis of genetic markers to identify subjects who will benefit from
 PT exercise - also assessing risk of cardiovascular disease from angiotensin
 PT -converting enzyme genotype.
 XX
 XX Disclosure; Page 29-32; 61pp; English.
 XX
 XX This is the human lipoprotein lipase (LPL) gene that encodes an enzyme
 CC (see AAM68154) that catalyzes the breakdown of triglycerides to release
 CC free fatty acids, and which may also be an important regulator of
 CC chylomicron metabolism. It is an object of the invention to identify
 CC individuals possessing a certain genotype and associated ailment, and to
 CC determine if the health of that individual can be improved by altering
 CC behavior. A claimed method comprises identifying individuals having a
 CC certain phenotype, determining the presence or absence of genetic markers
 CC associated with the phenotype, and instituting a lifestyle change to
 CC exploit or counteract the phenotype expressed by the gene marker. If the
 CC phenotype is hypertension, the gene marker is located at restriction
 CC sites (PvuII or HindIII) of the LPL gene locus and exercise training is
 CC instituted to decrease blood pressure. The gene marker can be identified
 CC by PCR amplification (see AAV41323-26) of the appropriate gene fragments.
 CC The general method can be used to identify subjects who will benefit most
 CC from physical exercise and also to identify those who are likely to be
 CC successful in sports
 XX
 XX SQ Sequence 3549 BP; 1021 A; 741 C; 805 G; 982 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: Length: 3549
 Score: 2385.00 Matches: 448
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0
 US-10-019-341-3 (1-448) x AAV41319 (1-3549)
 QY 1 AlaAspGlnArgAspPheIleAspIleGluSerIysPheAlaLeuArgThrProGlu 20
 DB 256 GCGGACCAAGAGAGATTATTCGACATCGAAGTAAATTGGCCCTAGAGACCCCTGAA 315
 QY 21 AspThrAlaGluAspThrCysHisLeuIleProGlyValAlaGluSerValAlaThrCys 40
 DB 316 GACACAGCTGAGACATTGCCACCTCATTCGCCGAGTAGACAGTCCGTGGCTACCTGT 375
 QY 41 HisPheAsnHisSerSerIysThrPheMetValIleHisGlyTrpThrValThrGlyMet 60
 DB 376 CATTTCAATCACAGCAGCAAAACCTTCATGGTGTATCCATGGCTGGACGGTAACAGGAATG 435
 QY 61 TyrGluSerTrpValProIysLeuValAlaAlaLeuTyrIysArgGluProAspSerAsn 80
 DB 436 TATGAGAGTGGGGCCAAACCTTGTGGCCGCCCTGTACAGAGAGAACCCAGATCCCAAT 495
 QY 81 ValIleValValAspTrpLeuSerArgAlaGlnGluHisTyrProValSerAlaGlyTyr 100
 DB 496 GTCAATTGGTGGACTGGCTGTCCGCGCTCAGGAGCATTAACCCAGTGTCCGCGGGCTAC 555
 QY 101 ThrLysLeuValGlyGlnAspValAlaArgPheIleAsnTrpMetGluGluPheAsn 120
 DB 556 ACCAAACTGGTGGACAGGATGTGGCCCGTTTATCAACTGGATGGAGGAGGATTAAAC 615
 QY 121 TyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeuGlyValAlaHisAlaAlaGlyIle 140
 DB 616 TACCCTCTGGACAAATGTCAATCTCTTGGGATACAGCCCTTGGAGCCCATGCTGCTGGCATT 675

QY 141 AlaGlySerLeuThrAsnLysLysValAsnArgIleThrGlyLeuAspProAlaGlyPro 160
 DB 676 GCAGGAAGTCTGACCAATAGAAAGTCAACAGAAATTACTGCGCTCGATCCAGCTGGACCT 735
 QY 161 AsnPheGluTyrAlaGluAlaProSerArgLeuSerProAspAspAlaAspPheValAsp 180
 DB 736 AACCTTTGAGTATGCAGAAAGCCCGAGTCGTCTTCTCTGATGATGAGATTTTGTAGAC 795
 QY 181 ValLeuHisThrPheThrArgGlySerProGlyVArgSerIleGlyIleGlnLysProVal 200
 DB 796 GTCTTACACACATTACACAGAGGTCCCTGGTTCGAAGCATTTGGAATCCAGAACCCAGTT 855
 QY 201 GlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGlu 220
 DB 856 GGGCATGTTGACATTTACCCGAATGGAGGTACTTTTCAGCCAGGATGTAAATTTGGAGAA 915
 QY 221 AlaIleArgValIleAlaGluArgGlyLeuGlyAspValAspGlnLeuValLysCysSer 240
 DB 916 GCTATCCCGCTGATTGCAGAGAGAGACTTGGCGATGTGGACCCAGCTAGTGAAGTCTCC 975
 QY 241 HisGluArgSerIleHisLeuPheIleAspSerLeuLeuAsnGluGluAsnProSerLys 260
 DB 976 CACGAGCCCTCCATTCATCTCTTCATCGACTCTCTGTTGAATGAAGAAATCCAAAGTAAG 1035
 QY 261 AlaTyrArgCysSerSerLysGluAlaPheGluLysGlyLeuCysLeuSerCysArgLys 280
 DB 1036 GCTTACAGGTGCAGTTCCTCCAGGAAGCCCTTCAGAAAGGCTCTGCTGAGTTGTAGAAG 1095
 QY 281 AsnArgCysAsnAsnLeuGlyTyrGluLeuAsnLysValArgAlaIysArgSerSerLys 300
 DB 1096 AACCGCTGCAACAATCTGGGCTATGAGATCAATAAGTCAGAGCCAAAGAGACGACAA 1155
 QY 301 MetTyrLeuLysThrArgSerGlnMetProTyrLysValPheHisTyrGlnValLysIle 320
 DB 1156 ATGTACTCTGAAGACTCGTTCTCAGATGCGCTTCAAAAGTCTTCCATTACCAAGTAAAGATT 1215
 QY 321 HisPheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGluIleSerLeuTyr 340
 DB 1216 CATTTTCTGGGACTGAGAGTGAACCCCATACCAATCAGGCTTTTGGAGATTTCTCTGTAT 1275
 QY 341 GlyThrValAlaGluSerGluAsnIleProPheThrLeuProGluValSerThrAsnLys 360
 DB 1276 GGCACCGTGGCGGAGAGTGAACAATCCCATTCACCTCGCTCGAAGTTTCCCAANTAAAG 1335
 QY 361 ThrTyrSerPheLeuIleTyrThrGluValAspIleGlyGluLeuLeuMetLeuLysLeu 380
 DB 1336 ACCTACTCTCTTCTTAATTTACACAGAGGTAGATATTGGAGAACTACTCATGTTTGAAGCTC 1395
 QY 381 LysTrpLysSerAspSerTyrPheSerTrpSerAspTrpTrpSerSerProGlyPheAla 400
 DB 1396 AATGAGAGAGTCAATTCATCTTGTAGCTGAGTGGTGGAGCAGTCCCGGCTTGGCC 1455
 QY 401 IleGlnLysIleArgValLysAlaGlyGluThrGlnLysLysValIlePheCysSerArg 420
 DB 1456 ATTCAAGATCAGAGTAAAGCAGGAGAGACTCAGAAAAGGTGATCTTCTGTCTAGG 1515
 QY 421 GluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHisAsp 440
 DB 1516 GAGAAAGTGTCTCATTTTGCAGAAAGGAAAGGACCTCGCGTATTGTGAAATGCCATGAC 1575
 QY 441 LysSerLeuAsnLysLysSerGly 448
 DB 1576 AAGTCTCTGAATAAGAAGTCAGGC 1599
 RESULT 2
 AAZ32183
 ID AAZ32183 standard; cDNA; 3549 BP.
 XX
 XX AAZ32183;
 XX
 XX 13-JAN-2000 (first entry)
 DT
 XX

DE Human lipoprotein lipase nucleotide sequence.
 XX Human; coding sequence polymorphism; vascular pathology gene;
 KW polymorphic site; phenotype correlation; forensic; paternity testing;
 KW medicine; genetic analysis; vascular disease; ds.
 XX Homo sapiens.
 XX WO9950454-A2.
 XX 07-OCT-1999.
 XX 26-MAR-1999; 99WO-US0006473.
 XX 01-APR-1998; 98US-00054272.
 XX (WHED) WHITEHEAD INST BIOMEDICAL RES.
 XX Lander ES, Daley GQ, Cargill M, Ireland JS, Rozen SG;
 XX WPI; 1999-620066/53.
 XX P-PSDB; AAY49564.
 XX Determination of polymorphisms in genes, especially those identifying
 XX predisposition to vascular disease.
 XX Claim 1; Fig 27; 134pp; English.
 XX AAZ32159 to AAZ32194 represent reference alleles for specifically claimed
 CC nucleic acid sequences from the present invention which comprise
 CC polymorphic sites as given in a table in the specification, selected from
 CC 92 single nucleotide polymorphisms in which the nucleotide at the
 CC polymorphic site is different from a nucleotide at the same site in a
 CC reference allele. The nucleic acids, and primers and probes, are used to
 CC identify polymorphisms, which may predispose an individual to disease,
 CC especially a vascular disease. They can also be used in phenotype
 CC correlations, forensics, paternity testing, medicine or genetic analysis.
 CC AA49550 to AA49573 represent the proteins which correspond to some of
 CC the reference alleles
 XX
 SQ Sequence 3549 BP; 1020 A; 739 C; 806 G; 984 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 4.04e-237 Length: 3549
 Score: 2385.00 Matches: 448
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0
 US-10-019-341-3 (1-448) x AAZ32183 (1-3549)
 QY 1 AlaAspGlnArgArgAspPheIleAspIleGluSerLysPheAlaLeuArgThrProGlu 20
 DB 256 GCCGACCAAGAGAGATTTATCGACATCGAAGATAAATTTGCCCTTAAGACCCCTGAA 315
 QY 21 AspThrAlaGluAspThrCysHisLeuIleProGlyValAlaGluSerValAlaThrCys 40
 DB 316 GACACACCTGAGGACATTTGCCACCTCATTTCCCGAGTAGCAGAGTCCGTGGCTACCTGT 375
 QY 41 HisPheAsnHisSerSerLysThrPheMetValIleHisGlyTrpThrValThrGlyMet 60
 DB 376 CATTTCAATCACAGCAGCAAAACCTTCATGGTGATCATCGCTGAGCGGTACAGGANTG 435
 QY 61 TyrGluSerTrpValProLysLeuValAlaAlaLeuTrpLysArgGluProAspSerAsn 80
 DB 436 TATGAGAGTGGGGTGCACAAACCTTTGTGGCGCCCTGTACAGAGAGAACACAGACTCCCAAT 495
 QY 81 ValIleValValAspTrpLeuSerArgAlaGlnGluHisTrpProValSerAlaGlyTyr 100
 DB 496 GTCAATGTGTGGTGGCTGTGTACGGGCTCAGAGCATTTACCCAGTGTCCGGGGGTAC 555
 QY 101 ThrLysLeuValGlyGlnAspValAlaArgPheIleAsnTrpMetGluGluGluPheAsn 120

RESULT 3
 ABL66907

DB 556 ACCAAACTGGTGGGACAGGATGTGGCCGGTTTATCACTGGATGGAGGAGGATTTAAC 615
 QY 121 TyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeuGlyAlaHisAlaGlyIle 140
 DB 616 TACCTCTGGACAATGTCCATCTCTTGGGATACAGCCTTGGAGCCCATGCTGTGGCATT 675
 QY 141 AlaGlySerLeuThrAsnLysLysValAsnArgIleThrGlyLeuAspProAlaGlyPro 160
 DB 676 GCAGGAAGTCTGACCAATTAAGAAAGTCAACAGAAATTAATGGCCCTCGATCCAGCTGGACCT 735
 QY 161 AsnPheGluTyrAlaGluAlaProSerArgLeuSerProAspAspAlaAspPheValAsp 180
 DB 736 AACTTTGAGTATGCAGAGCCCGAGTGTCTTCTCTCTGATGATGATGATGATGATGATGAT 795
 QY 181 ValLeuHisThrPheThrArgGlySerProGlyArgSerIleGlyIleGlnLysProVal 200
 DB 796 GTCTTACACACATTCACAGAGGTCCTCTGTGTCGAAAGCATTTGGAATCCAGAAACCATGTT 855
 QY 201 GlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGlu 220
 DB 856 GGGCATGTTGACATTTACCCGATGGAGGTACTTTTCAGCCAGGATGTAACTGGAGAA 915
 QY 221 AlalleArgValIleAlaGluArgGlyLeuGlyAspValAspGlnLeuValLysCysSer 240
 DB 916 GCTATCCGCGTATTCAGAGAGAGGACTTGGAGATGTGGACCCAGCTAGTGAAGTCTCTC 975
 QY 241 HisGluArgSerIleHisLeuPheIleAspSerLeuLeuAsnGluGluAsnProSerLys 260
 DB 976 CACGAGCGCTCATTCATCTCTTCATCGACTCTCTGTGTAATGAAGAAATCAAGTAAG 1035
 QY 261 AlaTyrArgCysSerSerLysGluAlaPheGluLysGlyLeuCysLeuSerCysArgLys 280
 DB 1036 GCTACAGCTGCAGTTCACAGGACCTTTGAGAAAGGCTCTGCTTGAGTTGTGAGAAAG 1095
 QY 281 AsnArgCysAsnAsnLeuGlyTyrGluIleAsnLysValArgAlaLysArgSerSerLys 300
 DB 1096 AACCGCTGCAACAATCTGGGCTATGAGATCAATAAAGTCAGAGCCAAAGAGCAGCAAA 1155
 QY 301 MetTyrLeuLysThrArgSerGlnMetProTyrLysValPheHisTyrGlnValLysIle 320
 DB 1156 ATGTACCTGAAGACTCGTTCTCAGATGCCCTACAAAGCTTCCATTACCAAGTAAAGATT 1215
 QY 321 HisPheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGluIleSerLeuTyr 340
 DB 1216 CATTTTCTGGGACTGAGAGTGAAACCCATACCAATCAGGCTTTCAGATTTCTCTGTAT 1275
 QY 341 GlyThrValAlaGluSerGluAsnIleProPheThrLeuProGluValSerThrAsnLys 360
 DB 1276 GGCACCGTGGCCGAGAGTGAGAACATCCCATTCATCTGCCCTGAAGTTTCCACAAATPAG 1335
 QY 361 ThrTyrSerPheLeuIleTyrThrGluValAspIleGlyGluLeuLeuMetLeuLysLeu 380
 DB 1336 ACCTACTCTCTTCCATTTTACAGAGGTAGATATTCGAGAACTACTCATGTTGAAGCTC 1395
 QY 381 LysTrpLysSerAspSerTyrPheSerTyrPheSerTrpSerSerProGlyPheAla 400
 DB 1396 AATGGAAGAGTGATTCATCTTGTAGCTGTGAGCTGTGGAGCAGTCCCGGCTTCGCC 1455
 QY 401 IleGlnValIleArgValLysAlaGlyGluThrGlnLysLysValIlePheCysSerArg 420
 DB 1456 ATTCAGAGATCAGAGTAAAGCAGGAGAGACTCAGAAAAAGGTGATCTTCTGTTCTAGG 1515
 QY 421 GluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHisAsp 440
 DB 1516 GAGAAAGTGTCTCATTTGGAGAAAGGAAAGGCCACCTGCGGTATTTGTGAAATGCCATGAC 1575
 QY 441 LysSerLeuAsnLysLysSerGly 448
 DB 1576 AAGTCTCTGAATTAAGAGTCAGGC 1599

Mon Oct 25 15:42:52 2004

us-10-019-341-3.rng

ID XX ABL66907 standard; DNA; 3549 BP.
XX AC ABL66907;
XX DT 15-MAY-2002 (first entry)
XX DE Lung cancer related gene sequence SEQ ID NO:5244.
XX KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
XX KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
XX KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
XX KW gene; ds.
XX OS Homo sapiens.
XX PN WO200194629-A2.
XX PD 13-DEC-2001.
XX PF 30-MAY-2001; 2001WO-US010838.
XX PR 05-JUN-2000; 2000US-0209473P.
XX PR 05-JUN-2000; 2000US-0209531P.
XX PR 18-SEP-2000; 2000US-0233133P.
XX PR 18-SEP-2000; 2000US-0233133P.
XX PR 20-SEP-2000; 2000US-0234009P.
XX PR 20-SEP-2000; 2000US-0234034P.
XX PR 20-SEP-2000; 2000US-0234052P.
XX PR 22-SEP-2000; 2000US-0234509P.
XX PR 22-SEP-2000; 2000US-0234567P.
XX PR 25-SEP-2000; 2000US-0234923P.
XX PR 25-SEP-2000; 2000US-0234924P.
XX PR 25-SEP-2000; 2000US-0235077P.
XX PR 25-SEP-2000; 2000US-0235082P.
XX PR 25-SEP-2000; 2000US-0235134P.
XX PR 25-SEP-2000; 2000US-0235280P.
XX PR 26-SEP-2000; 2000US-0235637P.
XX PR 26-SEP-2000; 2000US-0235638P.
XX PR 27-SEP-2000; 2000US-0235711P.
XX PR 27-SEP-2000; 2000US-0235720P.
XX PR 27-SEP-2000; 2000US-0235840P.
XX PR 27-SEP-2000; 2000US-0235863P.
XX PR 28-SEP-2000; 2000US-0236028P.
XX PR 28-SEP-2000; 2000US-0236032P.
XX PR 28-SEP-2000; 2000US-0236033P.
XX PR 28-SEP-2000; 2000US-0236034P.
XX PR 28-SEP-2000; 2000US-0236109P.
XX PR 28-SEP-2000; 2000US-0236111P.
XX PR 29-SEP-2000; 2000US-0236842P.
XX PR 29-SEP-2000; 2000US-0236891P.
XX PR 02-OCT-2000; 2000US-0237172P.
XX PR 02-OCT-2000; 2000US-0237173P.
XX PR 02-OCT-2000; 2000US-0237278P.
XX PR 02-OCT-2000; 2000US-0237294P.
XX PR 02-OCT-2000; 2000US-0237295P.
XX PR 02-OCT-2000; 2000US-0237316P.
XX PR 03-OCT-2000; 2000US-0237425P.
XX PR 03-OCT-2000; 2000US-0237598P.
XX PR 03-OCT-2000; 2000US-0237604P.
XX PR 03-OCT-2000; 2000US-0237606P.
XX PR 03-OCT-2000; 2000US-0237608P.
XX PR 01-NOV-2000; 2000US-0244867P.
XX PR 01-NOV-2000; 2000US-0245084P.
XX PA (AVAL-) AVALON PHARM.
XX PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
XX PI Sopnet DR, Weaver Z;
XX WPI; 2002-188264/24.
XX PT Screening for anti-neoplastic agent involves exposing cells to a chemical
agent to be tested for anti-neoplastic activity, and determining a change

PT in expression of a gene of a signature gene set.

XX Claim 1; SEQ ID NO 5244; 44pp; English.

XX The present invention describes a method (M1) for screening for an anti-

CC neoplastic agent. The method involves exposing cells to a chemical agent

CC to be tested for anti-neoplastic activity, determining a change in

CC expression of at least one gene (I) of a signature gene set, where (I)

CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664

CC to ABL70110), or is at least 95% identical to (S), where a change in

CC expression is indicative of anti-neoplastic activity. (I) has cytostatic

CC activity and can be used in gene therapy. M1 can be used for screening an

CC anti-neoplastic agent, and can be used to convey the chemical structure and/or

CC the data collected with respect to the anti-neoplastic agent as a result

CC of M1, and the data is sufficient to convey the chemical structure and/or

CC properties of the agent. M1 can be used in the treatment of cancer such

CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,

CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell

CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous

CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's

CC tumour

XX SQ Sequence 3549 BP; 1020 A; 739 C; 806 G; 984 T; 0 U; 0 Other;

Alignment Scores: 4.04e-237 Length: 3549

Pred. No.: 2385.00 Matches: 448

Score: 100.00% Conservativity: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-10-019-341-3 (1-448) x ABL66907 (1-3549)

QY 1 AlaAspGlnArgAspPheIleAspIleGluSerLysPheAlaLeuArgThrProGlu 20

DB 256 GCCGACCAAGAGAGATTTTATCGACATCGAAAGTAATTTGCCCTAGGACCCCTGAA 315

QY 21 AspThrAlaGluAspThrCysHisLeuIleProGlyValAlaGluSerValAlaThrCys 40

DB 316 GACACAGCTGAGGACACTTGCACCTCATTCGCGAGTAGCAGAGTCCGCTGCTACCTGT 375

QY 41 HisPheAsnHisSerSerLysThrPheMetValIleHisGlyTrpThrValThrGlyMet 60

DB 376 CATTTCAATCACAGCAGCAAAACCTTCATGCTGATCCATGCTGGACGTAACAGGAATG 435

QY 61 TyrGluSerTrpValProLysLeuValAlaAlaLeuTyrLysArgGluProAspSerAsn 80

DB 436 TATGAGAGTTGGTGCCAAACCTTGTCGCGCCCTGTACAGAGAGAACCCAGACTCCAAT 495

QY 81 ValIleValValAspTrpLeuSerArgAlaGlnGluHisTyrProValSerAlaGlyTyr 100

DB 496 GTCTTTGTGGTGGACTGGCTGTCCGCGCTCAGAGACATTTACCCAGTGTCCGCGGGCTAC 555

QY 101 ThrLysLeuValGlyGlnAspValAlaArgPheIleAsnTrpMetGluGluGluPheAsn 120

DB 556 ACCAAACTGGTGGACAGGATGTGGCCCGCTTTATCACTGGATGGAGGAGGAGTTAAC 615

QY 121 TyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeuGlyValAlaHisAlaGlyIle 140

DB 616 TACCCCTCTGGACAATGTCCATCTCTTGGGATACAGCCTTGAGGCCCATGTCTGGCATT 675

QY 141 AlaGlySerLeuThrAsnLysValAsnArgIleThrGlyLeuAspProAlaGlyPro 160

DB 576 GCAGGAAGTCTGACCAATAGAAAGTCAACAGAAATTTACTGGCTTCGATCCAGCTGGACCT 735

QY 161 AsnPheGluTyrAlaGluAlaProSerArgLeuSerProAspAlaAspPheValAsp 180

DB 736 AACTTTGAGTATGAGAAGCCCGAGTCGTCTTCTCTGATGATGAGATTTTGTAGAC 795

QY 181 ValLeuHisThrPheThrArgGlySerProGlyArgSerIleGlyIleGlnLysProVal 200

DB 796 GTCTTACACATTCACAGAGGGTCCCTGTGTCGAGCATTTGGATCCAGAACCACTT 855

QY 201 GlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGlu 220
Db 856 GGGCATGTTGACATTTTACCCGATGGAGGTACITTTTCAGCCAGGATGTAACATTGGAGAA 915
QY 221 AlaIleArgValIleAlaGluArgGlyLeuGlyAspValAspGlnLeuValCysCysSer 240
Db 916 GCTATCCGCTGATTTGAGAGAGAGGACTTTGGAGATGTGACAGCTAGTGAAGTCTCC 975
QY 241 HisGluArgSerIleHisLeuPheIleAspSerLeuLeuAsnGlnGluAsnProSerLys 260
Db 976 CACGAGCGCTCCATTCATCTCTTCATCGACTCTCTGTTGAATGAAGAAATCCAAAGTAAG 1035
QY 261 AlaTyrArgCysSerSerLysGluAlaPheGluLysGlyLeuCysLeuSerCysArgLys 280
Db 1036 GCCTACAGGTGCAGTTCCTCAAGGAAGCTTTTGAAAGGGCTCTGCTTGATTTGTAAGAG 1095
QY 281 AsnArgCysAsnAsnLeuGlyTyrGluIleAsnLysValArgAlaLysArgSerLys 300
Db 1096 AACCGCTGCACATCTGGCTATGAGATCAATAAAGTCAGAGCCAAAGAGACGACAAA 1155
QY 301 MetTyrLeuLysThrArgSerGlnMetProTyrLysValPheHisTyrGlnValLysIle 320
Db 1156 ATGTACTCTGAAGACTGTTCTCAGATGCCCTCAAAAGTCTTCCATTACCAAGTAAAGATT 1215
QY 321 HisPheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGluIleSerLeuTyr 340
Db 1216 CATTTTCTGGGACTGAGAGTGAACCCCATACCAATCAGCGCTTTGAGATTCTCTGAT 1275
QY 341 GlyThrValAlaGluSerGluAsnIleProPheThrLeuProGluValSerThrAsnLys 360
Db 1276 GGCACCGTGGCGAGAGTGAGAACATCCCATCTCTGCTGAAAGTTTCCACAAATAAG 1335
QY 361 ThrTyrSerPheLeuIleTyrThrGluValAspIleGlyGluLeuMetLeuLysLeu 380
Db 1336 ACCTACTCTCTCCTAATTTACAGAGAGTAGATATTGGAGAACTACTCATGTGTAAGTC 1395
QY 381 LysTyrLysSerAspSerTyrPheSerTyrPheSerTyrPheSerProGlyPheAla 400
Db 1396 AAATGGAGAGATGATTTCATCTTATGCTGGTCAGACTGTTGGAGCAGTCCCGGCTTCGCC 1455
QY 401 IleGlnLysIleArgValLysAlaGlyGluThrGlnLysLysValIlePheCysSerArg 420
Db 1456 ATTCAAGAGATCAGAGTAAAGCAGGAGAGACTCAGAAAAAGGTGATCTTCTGTTCTAGG 1515
QY 421 GluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHisAsp 440
Db 1516 GAGAAAGTGCTCATTTTGCAGAAAGGAAGGACCTCGCGTATTGTGAAATGCCATGAC 1575
QY 441 LysSerLeuAsnLysLysSerGly 448
Db 1576 AAGTCTCTGAATAAGAAAGTCAGGC 1599

RESULT 4

ABT10903

ID ABT10903 standard; cDNA; 3549 BP.

XX AC ABT10903;

XX XX 04-DEC-2002 (first entry)

DE DE Human breast cancer associated coding sequence SEQ ID NO: 1037.

XX XX Human; breast specific gene; breast cancer; differential expression;
KW KW cytosolic; gene therapy; gene; ss.
XX XX Homo sapiens.

OS OS WO200259271-A2.

XX PN 01-AUG-2002.

XX PD 25-JAN-2002; 2002WO-US002176.

XX XX

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SQ

Alignment Scores:

Pred. No.: 4.04e-237 Length: 3549

Score: 2385.00 Matches: 448

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-10-019-341-3 (1-448) x ABT10903 (1-3549)

QY 1 AlaAspGlnArgArgAspPheIleAspIleGluSerLysPheAlaLeuArgThrProGlu 20

Db 256 GCCGACCCAAAGAGAGATTTTATCGACATCGAAAGTAAATTTGCCCTAAGGACCCCTGAA 315

QY 21 AspThrAlaGluAspThrCysHisLeuIleProGlyValAlaGluSerValAlaThrCys 40

Db 316 GACACAGCTCAGGACACTTCCACCTCATTCGCGAGTAGCAGAGTCCGCGGTACTCTGT 375

QY 41 HisPheAsnHisSerSerLysThrPheMetValIleHisGlyTyrThrValThrGlyMet 60

Db 376 CATTTCAATCAGACAGCAAAACCTTCATGCTCATCCATCGCTGGAGGTAAACAGGATG 435

QY 61 TyrGluSerTyrValProLysLeuValAlaLeuTyrLysArgGluProAspSerAsn 80

Db 436 TATGAGAGTTGGTGCCAAACCTTGCGCGCCCTGTACAAGAGAGAACCCAGACTCCAAT 495

QY 81 ValIleValValAspTyrLeuSerArgAlaGlnHisTyrProValSerAlaGlyTyr 100

Db 496 GTCAATGTGTGGAGTGGTGTGTACGGGCTCAGGACATTACCCAGTGTCCGCGGTAC 555

QY 101 ThrLysLeuValGlyGlnAspValAlaArgPheIleAsnTyrMetGluGluPheAsn 120

Db 556 ACCAACTGGTGGACAGGATGTGGCCCGTTTATCACTGGATGGAGAGGAGTTAAC 615

QY 121 TyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeuGlyAlaHisAlaGlyIle 140

Db 616 TACCCCTGGCAATGTCCATCTCTTGGGATACAGCCTTGGAGCCCATCTGCTGGCATT 675

25-JAN-2001; 2001US-0263757P.
25-APR-2001; 2001US-0286090P.
23-MAY-2001; 2001US-0292517P.
(GENE-) GENE LOGIC INC.
Orr MS, Nation M, Diggans JC, Zeng W;
WPI; 2002-674803/72.
Diagnosing breast cancer in a patient comprises detecting the level of
gene expression in cell or tissue samples, where a differential gene
expression is indicative of breast cancer.

Claim 1; SEQ ID NO 1037; 260pp + Sequence Listing; English.

The present invention relates to methods of diagnosing breast cancer in a
patient, which comprise detecting the level of expression in a tissue
sample of two or more genes selected from those shown in ABT09867-
ABT1112, where a differential expression of the genes indicates breast
cancer. The methods are useful in diagnosing, treating, detecting the
progression, and in monitoring treatment of breast cancer in patients.
The methods are also useful as a screening tool for agents that modulate
the onset or progression of breast cancer. The breast cancer genes may be
used as diagnostic markers for the prediction or identification of the
malignant state of breast tissue, for confirming the type and progression
of cancer, and for drug screening and assays. The present sequence is a
coding sequence of the invention. Note: The sequence data for this patent
did not form part of the printed specification, but was obtained in
electronic format directly from WIPO at
ftp.wipo.int/pub.published_pct_sequences

Sequence 3549 BP; 1020 A; 739 C; 806 G; 984 T; 0 U; 0 Other;

QY 141 AlaGlySerLeuThrAsnLysLysValAsnArgGileThrGlyLeuAspProAlaGlyPro 160
 DB 676 GCAGGAAGCTGACCAATAGAAAGTCAACAGAAATTAAGTCTGCTCGATCCAGCTGACCT 735
 QY 161 AsnPheGluThrAlaGluAlaProSerArgLeuSerProAspAspAlaAspPheValAsp 180
 DB 736 AACTTTGAGTATGAGAAAGCCGAGTCTCTTCTCTGATGATGAGATTTGTAGAC 795
 QY 181 ValLeuHisThrPheThrArgGlySerProGlyArgSerIleGlyIleGlnLysProVal 200
 DB 796 GTCTTACACACATTCACAGAGGGTCCCTGGTGAAGCAATGGAAATCCAGAAACCAAGT 855
 QY 201 GlyHisValAspIleThrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGlu 220
 DB 856 GGGCATGTTGACATTTACCGAATGAGGAGTCTTTTCAGCCAGGATGTAACATTGGAGAA 915
 QY 221 AlaIleArgValIleAlaGluArgGlyLeuGlyAspValAspGlnLeuValLysCysSer 240
 DB 916 GCTATCCGCGTATGTCAGAGAGAGGACTTGGAGATGGACAGCTAGTGAAGTCTCC 975
 QY 241 HisGluArgSerIleHisLeuPheIleAspSerLeuLeuAsnGluGluAsnProSerLys 260
 DB 976 CACGAGCGCTCATCTCTCTTCATCGACTCTCTGTTGAATGAAGAAATCCAAAGTAA 1035
 QY 261 AlaTyrArgCysSerSerLysGluAlaPheGluLysGlyLeuCysLeuSerCysArgLys 280
 DB 1036 GCCTACAGTGCAGTTCACGGAAGCCCTTGGAAAGGCTCTGCTTGAGTTGTAGAAG 1095
 QY 281 AsnArgCysAsnAsnLeuGlyTyrGluLeuAsnLysValArgAlaArgSerSerLys 300
 DB 1096 AACCGCTGCAAACTCTGGCTATGAGATCAATAAAGTCAGAGCCCAAGAAAGAGCAGCAA 1155
 QY 301 MetTyrLeuLysThrArgSerGlnMetProTyrLysValPheHisTyrGlnValLysIle 320
 DB 1156 ATGTACCTGAAGACATGCTCTCAGAGGCCCTCAAAAGTCTTCATTACCAAGTAAAGATT 1215
 QY 321 HisPheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGluIleSerLeuTyr 340
 DB 1216 CATTTTCTGGAGCTGAGAGTGAACCCATACCAATCAGGCTTTGAGATTTCTCTGTAT 1275
 QY 341 GlyThrValAlaGluSerGluAsnIleProPheThrLeuProGluValSerThrAsnLys 360
 DB 1276 GGCACCGTGGCCGAGAGTGAAGACATCCCATTCCTGCTGCTGAGATTTCCCAAAATAG 1335
 QY 361 ThrTyrSerPheLeuIleTyrThrGluValAspIleGlyGluLeuLeuMetLeuLysLeu 380
 DB 1336 ACCTACTCTCTCTTAATTTACAGAGGTAGATATTGGAGAACTACTCATGTTGAAGCTC 1395
 QY 381 LysTyrLysSerAspSerTyrPheSerTyrPheSerAspTyrPheSerProGlyPheAla 400
 DB 1396 AATGGAGAGTGTATTCATCTTCTAGTGTGAGTGTGGAGCAGTCCCGCTTGGCC 1455
 QY 401 IleGlnLysIleArgValLysAlaGlyGluThrGlnLysLysValIlePheCysSerArg 420
 DB 1456 ATTCAAGATCATGAGTAAAGCAGGAGAGACTCAGAAAAGGTGATCTCTGTTAGG 1515
 QY 421 GluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHisAsp 440
 DB 1516 GAGAAAGTGTCATTTTGCAGAAAGGAAAGGACCTGGGTATTTGTGAAATGCCATGAC 1575
 QY 441 LysSerLeuAsnLysLysSerGly 448
 DB 1576 AAGTCTCTGAATAAGAGTCAGGC 1599
 RESULT 5
 ID ABT13006
 AC ABT13006 standard; DNA; 3549 BP.
 XX AC ABT13006;
 XX 30-JAN-2003 (first entry)
 XX Human lipoprotein lipase (LPL) gene.
 DB

XX
 KW Human; gene; ds; gene therapy; single nucleotide polymorphism; SNP;
 KW cytochrome C oxidase subunit Vb; COX6B; high serum cholesterol; GPI-1;
 KW N-acetylglucosaminyl transferase component; cardiovascular disease; HDL;
 KW glycosylphosphatidylinositol-1; low serum high density lipoprotein.
 XX Homo sapiens.
 XX
 FH Location/Qualifiers
 FT replace(280, A)
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 FT /note= "Single nucleotide polymorphism"
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 FT replace(579, A)
 FT /*tag= b
 FT /note= "Single nucleotide polymorphism"
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 FT replace(609, A)
 FT /*tag= c
 FT /note= "Single nucleotide polymorphism"
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 FT /note= "Single nucleotide polymorphism"
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 FT /note= "Single nucleotide polymorphism"
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 FT replace(1338, A)
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 FT /note= "Single nucleotide polymorphism"
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 FT /note= "Single nucleotide polymorphism"
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 FT /note= "Single nucleotide polymorphism"
 FT
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 FT /note= "Single nucleotide polymorphism"
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 FT
 FT replace(3272, C)
 FT /*tag= s
 FT /note= "Single nucleotide polymorphism"
 FT
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 FT
 FT replace(3447, A)
 FT /*tag= u
 FT /note= "Single nucleotide polymorphism"
 FT
 FT replace(3449, A)
 FT /note= "Single nucleotide polymorphism"
 FT
 FT variation

PT /*tag= v
 XX /note= "Single nucleotide polymorphism"

PN WO200272604-A2.

XX 19-SEP-2002.

XX 05-MAR-2002; 2002WO-US006728.

XX 09-MAR-2001; 2001US-00802640.

XX (SEQU-) SEQUENOM INC.

XX Braun A, Bansal A, Kleya PW;

XX WPI; 2002-750478/81.

XX P-PSDB; AA015884.

XX Detecting the presence or absence of an allelic variant of a polymorphic region of COX6B and/or GPI-1 gene, useful for detecting a predisposition to high serum cholesterol, low serum HDL and cardiovascular disease.

PS Disclosure; Page 111-113; 199pp; English.

XX The invention comprises methods of detecting the presence or absence of at least one allelic variant of a polymorphic region of a gene associated with cardiovascular disease. The invention specifically relates to detecting the region of a cytochrome C oxidase subunit VIB (COX6B) gene that is associated with high serum cholesterol, or the region of the N-acetylglucosaminyl transferase component glycosylphosphatidylinositol-1 (GPI-1) gene that is associated with low serum high density lipoprotein (HDL). The methods of the invention are useful for detecting a predisposition to high serum cholesterol, low serum HDL and cardiovascular disease. The methods are also useful for elucidating pathological pathways, developing diagnostic assays and new drug therapies for such disorders. The present DNA sequence represents a human gene associated with high serum cholesterol, low serum HDL and/or cardiovascular disease

SQ Sequence 3549 BP; 1020 A; 739 C; 806 G; 984 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4.04e-237 Length: 3549
 Score: 2385.00 Matches: 448
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-019-341-3 (1-448) x ABT13006 (1-3549)

QY 1 AlaAspGlnArgArgAspPheIleAspIleGluSerLysPheAlaLeuArgThrProGlu 20
 DB 256 GCGGACCAAGACAGAGATTTCGACATCGAAAGTAAATTTGCCCCTAAGACCCCTGAA 315
 QY 21 AspThrAlaGluAspThrCysHisLeuIleProGlyValAlaGluSerValAlaThrCys 40
 DB 316 GACACAGCTGAGGACACTGCCACCTCATTCGCCGAGTAGCAGATCCGCTGGCTTACCTGT 375
 QY 41 HisPheAsnHisSerSerLysThrPheMetValIleHisGlyTrpThrValThrGlyMet 60
 DB 376 CATTTCAATCACAGCAGCAAAACCTTCATGGTGATCCATCGCTGGACGGTAACAGGAATG 435
 QY 61 TyrGluSerTrpValProLysLeuValAlaLeuTyrLysArgGluProAspSerAsn 80
 DB 436 TATGAGAGTGGGTGCGCAAACTTTGGCCGCCCTGTACAAAGAGAGAACACAGACTCCAAT 495
 QY 81 ValIleValValAspTrpLeuSerArgAlaGlnGluHisTyrProValSerAlaGlyTyr 100
 DB 496 GTCAATGTGTGACTGGCTGTCACGGGCTCAGAGCAATTACCAAGTTCGCGGGGCTAC 555
 QY 101 ThrLysLeuValGlyGlnAspValAlaArgPheIleAsnTrpMetGluGluGluPheAsn 120

RESULT 6

ADM41259

ID ADM41259 standard; DNA; 3549 BP.

Db 556 ACCAACTGTGGGACAGGATGTGGCCCGGTTTATCACTGGATGGAGGAGGTTTAAAC 615
 QY 121 TyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeuGlyAlaHisAlaAlaGlyTle 140
 Db 616 TACCTCTGACCAATGTCCATCTCTTGGGATACAGCCCTTGGAGCCCATGTCTGGCATT 675
 QY 141 AlaGlySerLeuThrAsnLysLysValAsnArgIleThrGlyLeuAspProAlaGlyPro 160
 Db 676 GCAGGAAGTCTGACCAATAGAAAGTCAACAGAAATTACTGGCCCTCGATCCAGCTGGACCT 735
 QY 161 AsnPheGluTyrAlaGluAlaProSerArgLeuSerProAspAspAlaAspPheValAsp 180
 Db 736 AACTTTGAGTATGCAGAAGCCCGAGTCTCTCTCTGATGATGCAGATTGTAGAC 795
 QY 181 ValLeuHisThrPheThrArgGlySerProGlyArgSerIleGlyIleGlnLysProVal 200
 Db 796 GTCTTACACACATTCCACAGAGGTCCTCTGGTGGAAAGCAATTGGAAATCCAGAAACAGTT 855
 QY 201 GlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGlu 220
 Db 856 GGGCATGTTCATTTACCCGAATGGAGGTACTTTTCAGCCAGGATGTAACTTGGAGAA 915
 QY 221 AlalleArgValIleAlaGluArgGlyLeuGlyAspValAspGlnLeuValLysCysSer 240
 Db 916 GCTATCCGCGTGAATTCAGAGAGAGGACTTGGAGATGTGGACAGCTAGTGAAGTCTCC 975
 QY 241 HisGluArgSerIleHisLeuPheIleAspSerLeuLeuAsnGluGluAsnProSerLys 260
 Db 976 CACGAGCGCTCATTCATCTCTTCATGACTCTCTGTGTAATGAAGAAATCAAGTAAG 1035
 QY 261 AlaTyrArgCysSerSerLysGluAlaPheGluLysGlyLeuCysLeuSerCysArgLys 280
 Db 1036 GCCTACAGGTGCAGTTCCAGGAAGCCCTTCGAAAGGGCTCTGCTTGAGTTGTAGAAG 1095
 QY 281 AsnArgCysAsnAsnLeuGlyTyrGluIleAsnLysValaAlaLysArgSerSerLys 300
 Db 1096 AACCGCTCAACAATCTGGGCTATGAGATCAATAAAGTCAGAGCCCAAGAAAGCAGCAAA 1155
 QY 301 MetTyrLeuLysThrArgSerGlnMetProTyrLysValPheHisTyrGlnValLysIle 320
 Db 1156 ATGTACCTGAAGACTCGTTCTCAGATGCCCTACAAAGTCTTCCATTACCAAGTAAAGAT 1215
 QY 321 HisPheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGluIleSerLeuTyr 340
 Db 1216 CATTTTCTGGGACTGAGAGGTGAACCCATACCAATCAGGCTTGGAGCTTCTCTGTAT 1275
 QY 341 GlyThrValAlaGluSerGluAsnIleProPheThrLeuProGluValSerThrAsnLys 360
 Db 1276 GGCACCCGTGGCCGAGAGTGAGAACATCCCATTCCTCTGCTGAAGTTTCCACAAATAG 1335
 QY 361 ThrTyrSerPheLeuIleTyrThrGluValAspIleGlyGluLeuLeuMetLeuLysLeu 380
 Db 1336 ACCTACTCTCTCTTAATTTACAGAGGTAGATTATGGAGAACTTACTCATGTTGAAGCTC 1395
 QY 381 LysTrpLysSerAspSerTyrPheSerTrpSerAspTrpTrpSerSerProGlyPheAla 400
 Db 1396 AAATGGAAGAGTGATTTCATCTTAGCTGTGACAGCTGTGGAGCAGTCCCGGCTTCGCC 1455
 QY 401 IleGlnLysIleArgValLysAlaGlyGluThrGlnLysLysValIlePheCysSerArg 420
 Db 1456 ATTCAAGAGATCAGAGTAAAGCAGGAGAGACTCAGAAAAAGGTGATCTTCTGTCTAGG 1515
 QY 421 GluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHisAsp 440
 Db 1516 GAGAAAGTCTCTCATTTGCAAGAAAGGACCCCTGCGGTATTTGTGTAATCCCATGAC 1575
 QY 441 LysSerLeuAsnLysLysSerGly 448
 Db 1576 AAGTCTCTGAATAAGAAGTCAGGC 1599

Mon Oct 25 15:42:52 2004

XX AC ADM41259;
 XX DT 03-JUN-2004 (first entry)
 XX DE Human lipoprotein lipase gene.
 XX KW Liver X receptor; lipoprotein lipase; antiatherosclerotic; nootropic;
 XX KW neuroprotective; litholytic; hepatotropic; antidiabetic; anorectic;
 XX KW antiinflammatory; 4-oxo-quinazoline; agonist; human; gene; enzyme; ds.
 XX OS Homo sapiens.
 XX PN EPI398032-A1.
 XX PD 17-MAR-2004.
 XX PF 10-SEP-2003; 2003EP-00020417.
 XX PR 10-SEP-2002; 2002EP-00020255.
 XX PH (PHEN-) PHENEX PHARM AG.
 XX PI Kober I, Albers M, Koegl M, Blume B, Deuschle U, Kremoser C;
 XX DR WPI; 2004-259060/25.
 XX DR GENBANK; M15856.
 XX PT Novel 4-oxo-quinazoline compound useful for treating atherosclerosis,
 XX PT Alzheimer's disease, gallstone disease, type II diabetes, lipid disorders,
 XX PT obesity, inflammatory or cardiovascular disorder.
 XX PS Disclosure; SEQ ID NO 15; 85pp; English.
 XX CC The present sequence is that of the human lipoprotein lipase (LPL) gene.
 XX CC This is an example of a gene that is regulated through binding of a liver
 XX CC X receptor (LXR) agonist to the LXR protein. The invention relates to 4-
 XX CC oxo-quinazolines which bind to LXR alpha or LXR beta, acting as selective
 XX CC agonists of the receptor. Such compounds are useful for treating a
 XX CC disease which is affected by cholesterol, triglyceride, bile acid,
 XX CC glucose or glucocorticoid levels in a mammal (especially a human). They
 XX CC can be used for the prevention or treatment of mammalian atherosclerosis,
 XX CC gallstone disease, lipid disorders, type 2 diabetes, Alzheimer's disease,
 XX CC skin disorders, inflammation, obesity or cardiovascular disorders such as
 XX CC coronary heart disease or stroke. The compounds can be used to block
 XX CC cholesterol absorption in a mammal, to treat obesity and to modulate a
 XX CC gene whose expression is regulated by LXR alpha or LXR beta (claimed).
 XX CC Expression of LPL is increased upon administration of a compound of the
 XX CC invention.
 XX SX Sequence 3549 BP; 1020 A; 739 C; 806 G; 984 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 4.04e-237 Length: 3549
 Score: 2385.00 Matches: 448
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 12 Gaps: 0
 US-10-019-341-3 (1-448) x ADM41259 (1-3549)
 QY 1 AlaAspGlnArgArgAspPheIleAspIleGluSerLysPheAlaLeuArgThrProGlu 20
 DB 256 GCCGACCAAGAGAGATTATCGACATCGAAAGTAAATTCGCCCTAAGGACCCCTGAA 315
 QY 21 AspThrAlaGluAspThrCysHisLeuIleProGlyValAlaGluSerValAlaThrCys 40
 DB 316 GACACAGCTGAGGACACTTGCACCTCATTCGCCGAGTAGCAGAGTCCGTGGCTACCTGT 375
 QY 41 HisPheHisSerSerLysThrPheMetValIleHisGlyTrpThrValThrGlyMet 60
 DB 376 CATTTCATCATCAGCAGCAGAACCTTCATGGTGATCCATGCTGGACCGTAAACAGGAATG 435

QY 61 TyrGluSerTrpValProLysLeuValAlaAlaLeuTyrLysArgGluProAspSerAsn 80
 DB 436 TATGAGATTGGTGGCCAAACCTTGTGGCCGCTGTACAAAGAGAACAGACTCCAAT 495
 QY 81 ValIleValValAspTrpLeuSerArgAlaGluGluHisTyrProValSerAlaGlyTyr 100
 DB 496 GTCATTGTGGTGGCTGTGTCCAGGCTCAGAGCATTTACCCAGTGTCCGCGGGCTAC 555
 QY 101 ThrLysLeuValGlyGlnAspValAlaArgPheIleAsnTrpMetGluGluGluPheAsn 120
 DB 556 ACCAAACTGGTGGACAGGATGTGCCCGGTTTATCACTGGATGGAGGAGAGTTTAAAC 615
 QY 121 TyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeuGlyAlaHisAlaAlaGlyIle 140
 DB 616 TACCTCTGGACATGTCATCTCTTGGATACAGCCTTGGAGCCCATGTCTGTGGCAT 675
 QY 141 AlaGlySerLeuThrAsnLysLysValAsnArgIleThrGlyLeuAspProAlaGlyPro 160
 DB 676 GCAGGAAGTCTGACCAATAGAAAGTCAACAGAATTACTGGCCTCGATCCAGCTGGACCT 735
 QY 161 AsnPheGluTyrAlaGluAlaProSerArgLeuSerProAspAspAlaAspPheValAsp 180
 DB 736 AACTTTGAGTATGCAGAAAGCCCGAGTCTCTTCTCTGATGATGCAGATTTTGTAGAC 795
 QY 181 ValLeuHisThrPheThrArgLysSerProGlyArgSerIleGlyIleGlnLysProVal 200
 DB 796 GTCTTACACATTCACCAGAGGGTCCCTCGTGAAGCATTTGAATCCAGAAACCGATT 855
 QY 201 GlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGlu 220
 DB 856 GGGCATGTTGACATTTACCCGAAATGGAGGTACTTTTTCAGCCAGGATGTAACTTGGAGAA 915
 QY 221 AlaIleArgValIleAlaGluArgGlyLeuGlyAspValAspGlnLeuValLysCysSer 240
 DB 916 GCTATCCCGGTGATTGACAGAGAGAGACCTTGGAGATGTGGACAGCTAGTGAAGTCTCC 975
 QY 241 HisGluArgSerIleHisLeuPheIleAspSerLeuLeuAsnGluGluAsnProSerLys 260
 DB 976 CACGAGGCTCCATTCATCTCTTCGACTCTCTGTTCATGAGAAATCCAGTAAG 1035
 QY 261 AlaTyrArgCysSerSerLysGluAlaPheGluLysGlyLeuCysLeuSerCysArgLys 280
 DB 1036 GCCTACAGGTGAGTTCCTCAAGGAGCCTTTGAAAGGGCTCTGTGAGTTGTAGAAAG 1095
 QY 281 AsnArgCysAsnAsnLeuGlyTyrGluIleAsnLysValArgAlaLysArgSerSerLys 300
 DB 1096 AACCGCTGCAACAATCTGGGCTATGAGATCAATAAAGTCAGACCCAAAGAGCAGCAAA 1155
 QY 301 MetTyrLeuLysThrArgSerGlnMetProTyrLysValPheHisTyrGlnValLysIle 320
 DB 1156 ATGTACTGAGAGTCTGTTCTCAGATGCCCTACAAAGTCTTCCATTACCAAGTAAGATT 1215
 QY 321 HisPheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGluIleSerLeuTyr 340
 DB 1216 CATTTCCTGGAGTGAAGACCCATACCAATCAGGCCCTTTGAGATTTCTGTAT 1275
 QY 341 GlyThrValAlaGluSerGluAsnIleProPheThrLeuProGluValSerThrAsnLys 360
 DB 1276 GGCACCGTGGCCGAGGTGAGAACATCCCATTCATCTGCTGAAGTTTCCACAAATAAG 1335
 QY 361 ThrTyrSerPheLeuIleTyrThrGluValAspIleGlyGluLeuLeuMetLeuLysLeu 380
 DB 1336 ACCTACTCTCTCTTAATTTACACAGAGGTAGATATTGGAGAACTACTCATGTGAGAGCTC 1395
 QY 381 LysTrpLysSerAspSerTyrPheSerTrpSerAspTrpTrpSerSerProGlyPheAla 400
 DB 1396 AAATGGAGAGTGAATTCATCTTTAGCTGGTCAGACTGTGGAGCAGCTCCCGGCTCGCC 1455
 QY 401 IleGlnLysIleArgValLysAlaGlyGluThrGlnLysLysValIlePheCysSerArg 420
 DB 1456 ATTCAAGATCAGAGTAAAGCAGGAGAGACTCAGAAAAAGGTGATCTTCTGTCTTAGG 1515

QY 421 GluLysValSerHisLeuGlnLysGlyAlaProAlaValPheValLysCysHisAsp 440
 Db 1516 GAGAAAGTGCTCTATTGTCAGAAAGGAAAGGACCTCGGTATTGTGAAATGCCATGAC 1575
 QY 441 LysSerLeuAsnLysLysSerGly 448
 Db 1576 AAGTCTCTGAATAAGAGTCAAGC 1599

RESULT 7

ADQ23742

ID ADQ23742 standard; DNA; 4314 BP.

XX

AC ADQ23742;

XX

DT 26-AUG-2004 (first entry)

XX

DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6562.

XX

KW soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;

KW ds.

XX

OS Homo sapiens.

XX

PN WO2004048938-A2.

XX

PD 10-JUN-2004.

XX

PF 26-NOV-2003; 2003WO-US038193.

XX

PR 26-NOV-2002; 2002US-0429739P.

XX

PA (PROT-) PROTEIN DESIGN LABS INC.

XX

PI Aziz N, Ginsburg WM, Zlotnik A;

XX

WPI; 2004-441208/41.

XX

DR

XX

PT Early detection of soft tissue sarcoma comprises determining expression

PT of a gene in a first soft tissue sample and a normal soft tissue sample

PT and comparing the gene expression, also useful in treating soft tissue

PT sarcoma.

XX

PS Example 2; SEQ ID NO 6562; 210pp; English.

XX

CC The invention relates to a novel method for detecting soft tissue sarcoma

CC which comprises obtaining a first soft tissue sample from an individual

CC and a normal soft tissue sample from the same or different individual,

CC determining the expression of a gene in both samples and comparing the

CC expression of the gene in both soft tissue samples, where a higher level

CC of protein expression in the first soft tissue sample indicates the

CC presence of soft tissue sarcoma. The method of the invention has

CC cytotostatic applications and may be useful for detecting soft tissue

CC sarcoma, possibly via gene therapy or vaccine production. The nucleic

CC acid sequences may be useful in diagnostic and screening applications.

CC The current sequence is that of a human soft tissue sarcoma-upregulated

CC DNA of the invention. The current sequence is not shown within the

CC specification per se but was submitted in CD format by the inventor.

XX

SQ Sequence 4314 BP; 1314 A; 895 C; 981 G; 1124 T; 0 U; 0 Other;

XX

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

US-10-019-341-3 (1-448) x ADQ23742 (1-4314)

QY 1 AlaAspGlnArgAspPheIleAspIleGluSerLysPheAlaLeuArgThrProGlu 20

Db 750 GCCGACCAAGAGAGATTATTATCGACATCGAAAGTAAATTTGCCCTAAGACCCCTGAA 809

QY 21 AspThrAlaGluAspThrCysHisLeuIleProGlyValAlaGluSerValAlaThrCys 40
 Db 810 GACACAGCTGAGGACACTTGCACACTCATTTCCCGAGTAGACAGAGTCCGTGGCTACCTGT 869
 QY 41 HisPheAsnHisSerSerLysThrPheMetValIleHisGlyTrpThrValThrGlyMet 60
 Db 870 CATTTCAATCACAGCAGCAAAACCTTCATGGTGATCCATGGCTGGACGGTAACAGGAATG 929
 QY 61 TyrGluSerTrpValProLysLeuValAlaAlaLeuTyrLysArgGluProAspSerAsn 80
 Db 930 TATGAGAGTTGGTGCCAAACTTGTGGCGCCCTGTACAAGAGAGAACACAGACTCCAAT 989
 QY 81 ValIleValValAspTrpLeuSerArgAlaGlnGluHisTyrProValSerAlaGlyTyr 100
 Db 990 GTCAATTGTGGTGGACTGGCTGTACGGGGTCAAGAGCATTTACCCAGTGTCCGGGGCTAC 1049
 QY 101 ThrLysLeuValGlyGlnAspValAlaArgPheIleAsnTrpMetGluGluGluPheAsn 120
 Db 1050 ACCAAACTGGTGGACAGGATGTGGCCGGTTTATCAACTGGATGGAGGAGGATTAAAC 1109
 QY 121 TyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeuGlyAlaHisAlaGlyIle 140
 Db 1110 TACCTCTGGACATGTCCATCTCTGGGATACAGCTTTGGAGCCCATCTGTGGCAAT 1169
 QY 141 AlaGlySerLeuThrAsnLysLysValAsnArgIleThrGlyLeuAspProAlaGlyPro 160
 Db 1170 GCAGGAAGTCTGACCAATAAGAAAGTCAACAGAAATTTACTGGCTCGATCCAGCTGGACT 1229
 QY 161 AsnPheGluTyrAlaGluAlaProSerArgLeuSerProAspAspAlaAspPheValAsp 180
 Db 1230 AACTTTGAGTATGCAGAAAGCCCGAGTCTCTTTCTCTGATGATGCAGATTTGTAGAC 1289
 QY 181 ValLeuHisThrPheThrArgGlySerProGlyArgSerIleGlyIleGlnLysProVal 200
 Db 1290 GTCTTACACATTCACCAGAGGGTCCCTCTGGTGAAGCATTTGGAATCCAGAAACAGTT 1349
 QY 201 GlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGlu 220
 Db 1350 GGGCATGTGACATTTACCCGAATGGAGTACTTTTCAGCCAGGATGTAACATTGGAGAA 1409
 QY 221 AlaIleArgValIleAlaGluArgGlyLeuGlyAspValAspGlnLeuValLysCysSer 240
 Db 1410 GCTATCCGCTGATGTCAGAGAGAGACTTGGAGATGTGGACCACTAGTAGAGTGCTCC 1469
 QY 241 HisGluArgSerIleHisLeuPheIleAspSerLeuLeuAsnGluGluAsnProSerLys 260
 Db 1470 CACAGCGCTCCATTCATCTCTTCATGACTCTCTGTGATGAAGAAATCCAAAGTAAG 1529
 QY 261 AlaTyrArgCysSerSerLysGluAlaPheGluLysGlyLeuCysLeuSerCysArgLys 280
 Db 1530 GCCTACAGGTGAGTTCACAGGAGCCCTTGAGAAAGGGCTCTCTGTGAGTTGTAGAAAG 1589
 QY 281 AsnArgCysAsnAsnLeuGlyTyrGluIleAsnLysValArgAlaLysArgSerSerLys 300
 Db 1590 AACCGCTGCAACAATCTGGGCTATGAGATCAATAAAGTCAGAGCCAAAGAGACAGCAA 1649
 QY 301 MetTyrLeuLysThrArgSerGlnMetProTyrLysValPheHisTyrGlnValLysIle 320
 Db 1650 ATGTACTGAAGACTCGTTCTCAGATGCCCTACAAAGTCTTCCATTACCAAGTAAGATT 1709
 QY 321 HisPheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGluIleSerLeuTyr 340
 Db 1710 CATTTTCTGGGACTGAGAGTGAACCCATACCAATCAGCCCTTTGAGATTTCTCTGTAT 1769
 QY 341 GlyThrValAlaGluSerGluAsnIleProPheThrLeuProGluValSerThrAsnLys 360
 Db 1770 GGCACCGTGGCCGAGAGTGAAGAACATCCCATTCACCTCGCTGAAAGTTCCACAAATAG 1829
 QY 361 ThrTyrSerPheLeuIleTyrThrGluValAspIleGlyGluLeuMetLeuLysLeu 380
 Db 1830 ACTACTCTCTTAATTTACACAGAGGTAGATATTGGAGAACTACTCATGTTTGAAGCTC 1889

QY 381 LysTrpLysSerAspSerTrpPheSerTrpSerAspTrpTrpSerProGlyPheAla 400
 Db 1471 AAATGGAGAGTGTATCATCTTAGCTGGTGCAGACTGGTGGAGAGTCCCGGCTTCGCC 1530
 QY 401 IleGlnLysLysLeuValLysAlaGlyGluThrGlnLysLysValLysPheCysSerArg 420
 Db 1531 ATTGAGAGATCAGAGTAAAGCAGGAGAGACTCAGAAAAAGGTGATCTTCTGTTCTAGG 1590
 QY 421 GluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHisAsp 440
 Db 1591 GAGAAAGTGCTCATTTGCAGAAAGGAAGGCACCTGCGGTATTGTGAAATGCCATGAC 1650
 QY 441 LysSerLeuAsnLysLysSerGly 448
 Db 1651 AAGTCTCTGAATAGAAAGTCAGGC 1674

RESULT 9

ADB47407

ID ADB47407 standard; cDNA; 4075 BP.

XX ADB47407;

XX 04-DEC-2003 (first entry)

XX Human cDNA upregulated in dendritic cells SEQ ID NO 107.

XX ss; gene; human; dendritic cells; high throughput; cancer;

XX infectious disease; autoimmune disease; allergy;

XX graft versus host disease; vaccine enhancing; gene therapy.

XX Homo sapiens.

XX US2003134283-A1.

XX 17-JUL-2003.

XX 03-OCT-2001; 2001US-00971392.

XX 03-OCT-2000; 2000US-0237652P.

XX (PETE/) PETERSON D P.

XX (PEAR/) PEARSON C I.

XX (COCK/) COCKS B G.

XX Peterson DP, Pearson CI, Cocks BG;

XX WPI; 2003-662509/62.

XX Claim 1; SEQ ID NO 107; 28pp; English.

XX The invention relates to a combination comprising cDNAs that are
 CC differentially expressed in dendritic cells (DC). Also included is a high
 CC throughput method for detecting differential expression of one or more
 CC cDNAs in a sample containing nucleic acids. The combination is useful for
 CC preparing a composition for diagnosing, treating and monitoring the
 CC treatment of cancer, infectious disease, autoimmunity, allergy or graft
 CC versus host disease, or for enhancing a vaccine. The present sequence
 CC represents a human cDNA upregulated in dendritic cells. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format directly from USPTO
 CC at seqdata.uspto.gov/sequence.html?docID=20030134283.

SQ Sequence 4075 BP; 1168 A; 848 C; 938 G; 1121 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1-12e-235 Length: 4075

Score: 2372.00 Matches: 448

Percent Similarity: 99.78% Conservative: 0
 Best Local Similarity: 99.78% Mismatches: 0
 Query Match: 99.45% Indels: 1
 DB: 10 Gaps: 0

US-10-019-341-3 (1-448) x ADB47407 (1-4075)

QY 1 AlaAspGlnArgArgAspPheIleAspIleGluSerLysPheAlaLeuArgThrProGlu 20
 Db 750 GCCGACCAAGAGAGATTTATCGACATCGAAGTAATTTGCCCTTAAGGACCCCTGAA 809
 QY 21 AspThrAlaGluAspThrCysHisLeuIleProGlyValAlaGluSerValAlaThrCys 40
 Db 810 GACACAGCTGAGGACACTTCCACCTCATTCGCGAGTAGCAGAGTCCGTGGCTACTGT 869
 QY 41 HisPheAsnHisSerSerLysThrPheMetValIleHisGlyTrpThrValThrGlyMet 60
 Db 870 CATTTCAATCACAGCAGCAAAACCTTCATGGTGATCCATGGCTCGACGGTAACAGGAATG 929
 QY 61 TyrGluSerTrpValProLysLeuValAlaAlaLeuTyrLysArgGluProAspSerAsn 80
 Db 930 TATGAGAGTTGGTGCCAAACTTGTGGCGCCCTGTACAAGAGAGAACCCAGACTCCAAT 989
 QY 81 ValIleValValAspTrpLeuSerArgAlaGlnGluHisTyrProValSerAlaGlyTyr 100
 Db 990 GTCAATTGTGGTGGACTGGCTGTACGGGCTCAGGAGCATTACCCAGTGTCCGCGGCTAC 1049
 QY 101 ThrLysLeuValGlyGlnAspValAlaArgPheIleAsnTrpMetGluGluPheAsn 120
 Db 1050 ACCAACTGGTGGGACAGATGTGGCCGGTTTATCACTGGATGGAGGAGGTTTAAAC 1109
 QY 121 TyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeuGlyAlaHisAlaAlaGlyIle 140
 Db 1110 TACCCTCTGGACAATGTCCATCTCTGGGATACAGCTTGGAGCCCATGCTCTGGCAAT 1169
 QY 141 AlaGlySerLeuThrAsnLysLysValAsnArgIleThrGlyLeuAspProAlaGlyPro 160
 Db 1170 GCAGGAAGTCTGACCAATAAGAAAGTCAACAGATTACTGGCTCGATCCAGTGGACCT 1229
 QY 161 AsnPheGluTyrAlaGluAlaProSerArgLeuSerProAspAspAlaAspPheValAsp 180
 Db 1230 AACTTTGAGTAGCAGAAAGCCCGAGTGTCTTCTCTCGATGATGCAGATTTTGTAGAC 1289
 QY 181 ValLeuHisThrPheThrArgGlySerProGlyArgSerIleGlyIleGlnLysProVal 200
 Db 1290 GTCTTACACATTCACCAGAGGTCCTCGTGGTGAAGCATTTGGATCCAGATAGTGAAGT 1349
 QY 201 GlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGlu 220
 Db 1350 GGGCATGTTGACATTTACCCGAATGGAGGTACTTTTCAGCCAGGATGTAACTTTGGAGAA 1409
 QY 221 AlaIleArgValIleAlaGluArgGlyLeuGlyAspValAspGlnLeuValLysCysSer 240
 Db 1410 GCTATCCGCGTGATTGCAGAGAGGACTTGGAGATGTGGACAGCTAGTGAAGTGTCC 1469
 QY 241 HisGluArgSerIleHisLeuPheIleAspSerLeuLeuAsnGluGluAsnProSerLys 260
 Db 1470 CACGAGCGCTCCATTCATCTCTTCATCGACTCTCTGTGTAATGAAGAAATTCGAAGTAAG 1529
 QY 261 AlaTyrArgCysSerSerLysGluAlaPheGluLysGlyLeuCysLeuSerCysArgLys 280
 Db 1530 GCCTACAGGTGCAATTCGAAGGAGCCTTTGAGAAAGGCTCTGCTTGAGTTGTAGAAAG 1589
 QY 281 AsnArgCysAsnAsnLeuGlyTyrGluIleAsnLysValArgAlaLysArgSerSerLys 300
 Db 1590 AACCGCTGCAACAATCTGGGCTATGAGATCAATAAAGTCAGACCCAAAAAGACAGCAAA 1649
 QY 301 MetTyrLeuLysThrArgSerGlnMetProTyrLysValPheHisTyrGlnValLysIle 320
 Db 1650 ATGTACCTGAGACACCTGTTCTCAGATGCCCTACAAAGTCTTCATTACCAAGTAAAGATT 1709
 QY 321 HisPheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGluIleSerLeuTyr 340

CC progression of a toxic response, predicting the cellular pathways that a
CC compound modulates in a cell, and identifying an agent that modulates at
CC least one activity of a protein. The method and compositions of the
CC present invention using a database of genes having liver toxin-induced
CC differential expression, are useful in identifying toxicity markers in
CC liver tissues or cells for drug screening and toxicity assays. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 3617 BP; 1049 A; 780 C; 812 G; 976 T; 0 U; 0 Other;

Alignment Scores: Length: 3617
Pred No.: 1,48e-221 Matches: 416
Score: 2235.50 Conservativity: 17
Percent Similarity: 96.65% Mismatches: 14
Best Local Similarity: 92.86% Indels: 1
Query Match: 93.73% Gaps: 1
DB: 10

US-10-019-341-3 (1-448) x ADB58065 (1-3617)
QY 1 AlaAspGlnArgArgAspPheIleAspIleGluSerLysPheAlaLeuArgThrProGlu 20
DB 256 GCAGACGGGGGAGAGATTTCTCAGACATCGAAGATTAATTTCCCTAAGGACCCCTGAA 315
QY 21 AspThrAlaGluAspThrCysHisLeuIleProGlyValAlaGluSerValAlaThrCys 40
DB 316 GACACAGCTGAGGACATCTGTCTGATTCCTGGATTAGCAGACTCTGTCTAACTGC 375
QY 41 HisPheAsnHisSerSerLysThrPheMetValIleHisGlyTrpThrValThrGlyMet 60
DB 376 CACTTCAACACACAGCAGCAAAACCTTTGTGGTGATCCATGGATGGACGGTGACGGAATG 435
QY 61 TyrGluSerTrpValProLysLeuValAlaAlaLeuTyrLysArgGluProAspSerAsn 80
DB 436 TATGAGAGTTGGGTGCCCAACCTTGTGGCTGCCCTATACAAAGAGAACTGACTCAAT 495
QY 81 ValIleValValAspTrpLeuSerArgAlaGlnGluHisTyrProValSerAlaGlyTyr 100
DB 496 GTCAATTGTAGTAGCTGGTTGTATCGGGCCCGCAGCAACATTTATCCAGTGTCTGGCGGTAT 555
QY 101 ThrLysLeuValGlyGlnAspValAlaArgPheIleAsnTrpMetGluGluGluPheAsn 120
DB 556 ACCAAGCTGTGGGAAATGATGTGGCCAGCTTCACTCACTGGTGGAGGAAGAAATTTAAC 615
QY 121 TyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeuGlyAlaHisAlaAlaGlyIle 140
DB 616 TACCCCTAGACAATGTCCACCTCTTAGGGGTACAGTCTTGAGGCCATGCTGCTGGCGTG 675
QY 141 AlaGlySerLeuThrAsnLysValAsnArgIleThrGlyLeuAspProAlaGlyPro 160
DB 676 GCAGGAAGTCTGACCAACAGAGGTCAATAGATTTACTGGCTTGGATCCAGCTGGGCT 735
QY 161 AsnPheGluTyrAlaGluAlaProSerArgLeuSerProAspAspAlaAspPheValAsp 180
DB 736 AACCTTGTAGTATGAGAGAGCCCTTAGTGCCTTTCTCTGATGATGGGATTTCTAGAT 795
QY 181 ValLeuHisThrPheThrArgGlySerProGlyArgSerIleGlyIleGlnLysProVal 200
DB 796 GTCTTACACACATTTACCAAGGGGTGCGCTCGAGTATTTGGATCCAGAACCCAGTA 855
QY 201 GlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGlu 220
DB 856 GGGCATTTGTATATTTATCCCAATGGAGGCACTTTCCAGCCAGGATGCAATCTGGAGAA 915
QY 221 AlaIleArgValIleAlaGluArgGlyLeuGlyAspValAsnGlnLeuValLysCysSer 240
DB 916 GCCATTCTGTAAATTCAGAGAGAGGGCTTGGAGATGTGGACCATGCTGTGAGTGTCTCG 975
QY 241 HisGluArgSerIleHisLeuPheIleAspSerLeuLeuAsnGluGluAsnProSerLys 260
DB 976 CACGAGCGCTCCATCCATCTCTTCAATGTGATCTCCCTGCTGATGATGAAGAAAAACCCCAAG 1035

DB 1710 CATTTTCTGGACTGAGAGTGAACCAATACCAATCAGGCTTTGAGATTTCTCTGTAT 1769
QY 341 GlyThrValAlaGluSerGluAsnIleProPheThrLeuProGluValSerThrAsnLys 360
DB 1770 GGCACCGTGGCGAGAGTGAACATCCCATTTCTCTGCTGAGTTTCCACAAATAAG 1829
QY 361 ThrTyrSerPheLeuIleTyrThrGluValAspIleGlyGluLeuMetLeuLysLeu 380
DB 1830 ACCTACTCTCTTCTTAATTTACACAGAGGTAGATATTGAGAACTACTCATGTGAAGTC 1889
QY 381 LysTrpLysSerAspSerTyrPheSerTrpSerAspTrpTrpSerProGlyPheAla 400
DB 1990 AAATGGAAGAGTATTCATCTTTAGCTGGTGCAGACTGGTGAGGAGTCCCGGCTTCGCC 1949
QY 401 Ile-GlnLysIleArgValLysAlaGlyGluThrGlnLysLysValIlePheCysSerAr 420
DB 1950 ATTGCAGAGATCAGAGTAAAGACGAGAGACTCAGAAAAGGTGATCTTCTGTCTAG 2009
QY 420 gGluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHisAs 440
DB 2010 GGAGAAAGTGTCTCATTTGCAGAAAGGAAAGGCACCTGCGGTATTTGTGAATGCCATGA 2069
QY 440 physSerLeuAsnLysLysSerGly 448
DB 2070 CAAGTCTCTGAATAAGAGTCAGGC 2094

RESULT 10
ADB58065
ID ADB58065 standard; DNA; 3617 BP.
XX
AC ADB58065;
XX
DT 04-DEC-2003 (first entry)
XX
DE Toxicity-related gene, SEQ ID 3091.
XX
KW Toxic; toxin; gene expression profile; hepatotoxicity; liver;
KW drug screening; toxicity assay; ds.
XX
OS Unidentified.
XX
PN WO2003064624-A2.
XX
PD 07-AUG-2003.
XX
PF 31-JAN-2003; 2003WO-US003194.
XX
PR 31-JAN-2002; 2002US-00060087.
PR 15-MAR-2002; 2002US-0364045P.
PR 15-MAR-2002; 2002US-0364055P.
PR 30-DEC-2002; 2002US-0436643P.
XX
PA (GENE-) GENE LOGIC INC.
XX
PI Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Elashoff M;
XX
XX WPI; 2003-689530/65.
XX
PT Predicting a toxic effect of a compound, useful in identifying toxicity
PT markers in liver tissues or cells for drug screening and toxicity assays,
PT comprises preparing gene expression profile of tissue or cells exposed to
PT the compound.
XX
PS Claim 1; SEQ ID NO 3091; 1156pp; English.
XX
XX The present invention relates to a method for predicting a toxic effect
CC of a compound. The method comprises preparing a gene expression profile
CC of a tissue or cell sample exposed to the compound, and comparing the
CC gene expression profile to a database comprising SEQ ID 1-4925, where
CC differential expression of the gene indicates at least one toxic effect.
CC The method is useful for predicting at least one toxic effect of a
CC compound, predicting hepatotoxicity or the progression of a toxic effect
CC of a compound, identifying an agent that modulates the onset or

CC encoding a polypeptide which is believed to be cytostatic,
CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The
CC composition and methods are useful for diagnosing, preventing and
CC treating diseases such as proliferative (e.g. cancer), inflammatory,
CC immune, metabolic, genetic, bacterial and viral diseases. The present
CC sequence represents a human secreted protein encoding sequence. The
CC present sequence is available on WIPWEB and is not in the specification.
XX
SQ Sequence 1584 BP; 450 A; 363 C; 388 G; 383 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3,52e-197 Length: 1584
Score: 1996.00 Matches: 387
Percent Similarity: 82.17% Conservative: 0
Best Local Similarity: 82.17% Mismatches: 84
Query Match: 83.69% Indels: 0
DB: 12 Gaps: 2

US-10-019-341-3 (1-448) x ADP28939 (1-1584)

Qy 1 AlaAspGlnArgArgAspPheIleAspIleGluSerLysPheAlaLeuArgThrProGlu 20
Db 82 GCCGACCAAGAGAGATTTATCGACATCGAAGTAATTTGCCCTAAGGACCCCTGAA 141
Qy 21 AspThrAlaGluAspThrCysHisLeuIleProGlyValAlaGluSerValAlaThrCys 40
Db 142 GACACAGCTGAGGACATTCGCCACCTCATTCGCGAGTAGCAGAGTCCGTGCTACCTGT 201
Qy 41 HisPheAnHisSerSerLysThrPheMetValIleHisGlyThrValThrGlyMet 60
Db 202 CATTTCAATACACAGCAGCAAAACCTTCATGGTGATCCATGGCTGGACGGTAACAGAATG 261
Qy 61 TyrGluSerTrpValProLysLeuValAlaAlaLeuTyrLysArgGluProAspSerAsn 80
Db 262 TATGAGAGTTGGTGCCAAACTTTGTGGCGCCCTGTACAGAGAGAACCCAGACTCCAAAT 321
Qy 81 ValIleValValAspTrpLeuSerArgAlaGlnGluHisTyrProValSerAlaGlyTyr 100
Db 322 GTCAATTTGTGGACTGGCTGTCCAGCGCTCAGGAGCAATTAACCTGTCGCGGGCTAC 381
Qy 101 ThrLysLeuValGlyGlnAspValAlaArgPheIleAsnTrpMetGluGluGluPheAsn 120
Db 382 ACCAAACTGGTGGAGCAGGATGGCGCGGTTTATCAACTGGATGAGGAGGAGTTTAAAC 441
Qy 121 TyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeuGlyAlaHisAlaAlaGlyIle 140
Db 442 TACCTCTTGACAAATGTCCATCTTTGGGATACAGCCTTGAGCCCATGCTGCTGGCAAT 501
Qy 141 AlaGlySerLeuThrAsnLysLysValAsnArgIleThrGlyLeuAspProAlaGlyPro 160
Db 502 GCAGGAAGTCTGACCAATAAGAAAGTCAACAGAAATTAATGCGCTCGATCCAGCTGGACCT 561
Qy 161 AsnPheGluTyrAlaGluAlaProSerArgLeuSerProAspAspAlaAspPheValAsp 180
Db 562 AACTTTGAGTATGAGAGAGCCCGAGTCGCTTTCTCTGATGATGACGATTTGTAGAC 621
Qy 181 ValLeuHisThrPheThrArgGlySerProGlyArgSerIleGlyIleGlnLysProVal 200
Db 622 GTCTTTACACATTCACGAGGGTCCCTGCTCGAAGCATTTGGAATCCAGAAACCAAGTT 681
Qy 201 GlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGlu 220
Db 682 GGGCATGTGTGACATTTACCCCAATGGAGGTACTTTTCAGCCAGGATGTAAATTTGGAGAA 741
Qy 221 AlaIleArgValIleAlaGluArgGlyLeuGly 231
Db 742 GCTATCCGCGTATTCAGAGAGAGGACTTTGGAGACATGCCAAATGAACACTCTTTGTG 801
Qy 232 -----AspValAspGlnLeuVal 237
Db 802 AATTCTCCCGAGATACAATCTTGTGCTCTTTTATCCAGATGTGGACAGCTAGT 861
Qy 238 LysCysSerHisGluArgSerIleHisLeuPheIleAspSerLeuLeuAsnGluAsn 257

Db 862 AAGTGTCCACGAGCGCTCCATTCTCTCTCATCGACTCTCTGTGTGATGAGAAAT 921
Qy 258 ProSerLysAlaTyrArgCysSerLysGluAlaPheGluLysGlyLeuCysLeuSer 277
Db 922 CCAAGTAAGCGCTACAGGTGCACTTCAGAGAGCCCTTTGAGAAGGGCTCTGCTTGA 981
Qy 278 CysArgLysAsnArgCysAsnAsnLeuGlyTyrGluIleAsnLysValArgAlaLysArg 297
Db 982 TGTAGAAGAAGCCGCTGCAACAATCTGGGCTATGAGATCAATAAGTCAGAGCCAAAGA 1041
Qy 298 SerSerLysMetTyrLeuLysThrArgSerGlnMetProTyrLysValPheHisTyrGln 317
Db 1042 AGCAGCAAAATGTACCTGAAGACTCGTTCAGAGTGCCTTCAAAAGTCTTCCATTACCA 1101
Qy 318 ValLysIleHisPheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGluIle 337
Db 1102 GTAAAGATTCATTTTCTGGGACTGAGAGTGAAACCCATACCAATCAGGCCTTTGAGAT 1161
Qy 338 SerLeuTyrGlyThrValAlaGluSerGluAsnIleProPheThrLeuProGluValSer 357
Db 1162 TCTCTGTATGCGACCGTGGCGAGAGTGAGAACATCCCATTCACCTCTG----- 1209
Qy 358 ThrAsnLysThrTyrSerPheLeuIleTyrThrGluValAspIleGlyGluLeuMet 377
Db 1209 ----- 1209
Qy 378 LeuLysLeuLysTyrLysSerAspSerTyrPheSerTrpSerAspTrpTrpSerPro 397
Db 1209 ----- 1209
Qy 398 GlyPheAlaIleGlnLysIleArgValLysAlaGlyGluThrGlnLysLysValIlePhe 417
Db 1210 -----GTGATCTTC 1218
Qy 418 CysSerArgGluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLys 437
Db 1219 TGTCTTAGGAGAAAGTGTCTCATTTGCGAGAAGGAAGGACCTCGGTATTTGTGAAA 1278
Qy 438 CysHisAspLysSerLeuAsnLysLysSerGly 448
Db 1279 TGCCATGACAGATCTCTGTAATAAGAGTCAGGC 1311

RESULT 12

AAZ33576/C
ID AAZ33576 standard; cDNA; 2939 BP.

XX AC AAZ33576;

XX 08-DEC-1999 (first entry)

DE Human breast tumour-associated EST 36.

XX Expressed sequence tag; EST; human; breast; cancer; cytostatic;
XX medicaments; gene therapy; treatment; fat metabolism; ss.
XX Homo sapiens.

XX DE19813835-AL.

XX 23-SEP-1999.

XX 20-MAR-1998; 98DE-01013835.

XX 20-MAR-1998; 98DE-01013835.

XX (META-) METAGEN GES GENOMFORSCHUNG MBH.

XX Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E, Rosenthal A;

XX WPI, 1999-528979/45.

XX Human nucleic acid sequences and protein products from normal breast

PT tissue, useful for breast cancer therapy.

PS Claim 3; 124-125; 206pp; German.

XX This invention describes novel human nucleic acid sequences from normal breast tissue which have cytostatic activity. The nucleic acid sequences can be used to produce and isolate full-length gene sequences. They can be used to express proteins, which can be used as tools to find an activity against breast cancer. The sequences can be used in sense or antisense form. They are especially useful for medicaments for gene therapy to treat breast cancer and for treating illnesses associated with fat metabolism. AA233541-233610 represent expressed sequence tags described in the method of the invention

SQ Sequence 2939 BP; 857 A; 635 C; 545 G; 902 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1,43e-165 Length: 2939
Score: 1696.00 Matches: 323
Percent Similarity: 99.69% Conservative: 0
Best Local Similarity: 99.69% Mismatches: 0
Query Match: 71.11% Indels: 1
DB: 2 Gaps: 0

US-10-019-341-3 (1-448) x AA233576 (1-2939)

QY 126 ValHisLeuLeuGlyTyrSerLeuGlyAlaHisAlaGlyLeuValGlySerLeuThr 145
DB GTCCATCTCTGGGATACAGCTTGGAGCCCATGCTGCTGGCAATTCAGAAAGTCTGACC 2880
QY 146 AsnLysLysVal-AsnArgIleThrGlyLeuAspProAlaGlyProAsnPhelGlyTyrAl 165
DB AATAAGAAAGTTCACACAAATTTACTGGCTCGATCCAGCTGAGCTAACTTGGATGTC 2820
QY 165 aGluAlaProSerArgLeuSerProAspAspAlaAspPheValAspValLeuHisThrPh 185
DB AGAAGCCCGAGTGGTCTTCTCTGATGTCAGATTTGTAGACGCTTACACACATT 2760
QY 185 eThrArgGlySerProGlyArgSerIleGlyLeuGlyProValGlyHisValAspIl 205
DB CACCAGAGGGTCCCTGGTGAAGCATTTGGATCCAGAAACAGTTGGCGATGTGACAT 2700
QY 205 eTyrProAsnGlyThrPheGlnProGlyCysAsnIleGlyLeuAlaIleArgValIl 225
DB TTACCCGAATGGAGGTACTTTTCAGCCAGGATGTAACATTCGAGAAGCTATCCCGGTGAT 2640
QY 225 eAlaGluArgGlyLeuGlyAspValAspGlnLeuValLysCysSerHisGluArgSerIl 245
DB TGCAGACAGAGGACTTGGAGATGTGGACCACTAGTGAAGTGCTCCACAGCGCTCCAT 2580
QY 245 eHisLeuPheIleAspSerLeuLeuAsnGluGluAsnProSerLysAlaTyrArgCysSe 265
DB TCATCTCTTCATCGACTCTCTGTGAATGAAGAAATCCAGTAAGCCCTACAGGTGCAG 2520
QY 265 rSerLysGluAlaPheGlyLeuGlyLeuSerCysArgLysAsnArgCysAsnAs 285
DB TTCCAGGAAGCCTTTGAGAAAGGCTCTCTGAGTTGTAGAAGAACCGCTGCACAA 2460
QY 285 nLeuGlyTyrGluIleAsnLysValArgAlaLysArgSerSerLysMetTyrLeuLysTh 305
DB TCTGGCTATGAGATCAATAAGTCAGAGCCAAAGAGCAGCAAAATGTACCTGAAGAC 2400
QY 305 rArgSerGlnMetProTyrLysValPheHisTyrGlnValLysIleHisPheSerGlyTh 325
DB TCGTTCTCAGATGCCCTACAAAGTCTTCCATTACCAAGTAAGATTCATTTTCTGGGAC 2340
QY 325 rGluSerGluThrHisThrAsnGlnAlaPheGluIleSerLeuTyrGlyThrValAlaGl 345
DB TGAGAGTGAACCCCATACCAATCAGGCCCTTTCAGATTTCTGTATGGCAGCGTGCCCA 2280
QY 345 uSerGluAsnIleProPheThrLeuProGluValSerThrAsnLysThrTyrSerPheLe 365
DB GAGTGGAACATCCCATTCCTACTGCTGAGGTTTCCACAAATAAGACCTACTCTCTCT 2220

QY 365 uIleTyrThrGluValAspIleGlyGluLeuLeuMetLeuLysLeuLysTyrLysSerAs 385
DB AATTTACACAGAGGTAGATATTGGAGAACTACTCATGTTGAAGCTCAATGGAGAGTGA 2160
QY 385 pSerTyrPheSerTyrPheSerTrpTrpSerSerProGlyPheAlaIleGlnLysIleAr 405
DB TTCACTACTTTTAGCTGGTTCAGACTGGTGGAGCAGTCCCGGCTTCGCCATTCAGAGATCAG 2100
QY 405 gValLysAlaGlyGluThrGlnLysLysValIlePheCysSerArgGluLysValSerHi 425
DB AGTAAAGCAGGAGAGACTCAGAAAAAGGTGATCTTCTGTCTAGGAGAAAGTCTCA 2040
QY 425 sLeuGlnLysGlyLysAlaProAlaValPheValLysCysHisAspLysSerLeuAsnLy 445
DB TTTGCAGAAAGGAAGGACCTGGCTGATTTGTGAATGCCATGACAGTCTCTGAATAA 1980
QY 445 sLysSerGly 448
DB 1979 GAAGTCAGGC 1970

RESULT 13

AA233605
ID AA233605 standard; cDNA; 2933 BP.

XX AC AA233605;

XX DT 08-DEC-1999 (first entry)

XX DE Human breast tumour-associated EST 65.

XX KW Expressed sequence tag; EST; human; breast; cancer; cytostatic; medicaments; gene therapy; treatment; fat metabolism; ss.

XX OS Homo sapiens.

XX PN DE19813835-A1.

XX PD 23-SEP-1999.

XX PF 20-MAR-1998; 98DE-01013835.

XX PR 20-MAR-1998; 98DE-01013835.

XX PA (META-) METAGEN GES GENOMFORSCHUNG MBH.

XX PI Specht T, Hinzmann B, Schmitt A, Pillarsky C, Dahl E, Rosenthal A; WPI; 1999-528979/45.

XX PT Human nucleic acid sequences and protein products from normal breast tissue, useful for breast cancer therapy.

XX PS Claim 3; 153-154; 206pp; German.

XX CC This invention describes novel human nucleic acid sequences from normal breast tissue which have cytostatic activity. The nucleic acid sequences can be used to produce and isolate full-length gene sequences. They can be used to express proteins, which can be used as tools to find an activity against breast cancer. The sequences can be used in sense or antisense form. They are especially useful for medicaments for gene therapy to treat breast cancer and for treating illnesses associated with fat metabolism. AA233541-233610 represent expressed sequence tags described in the method of the invention

SQ Sequence 2933 BP; 902 A; 545 C; 635 G; 851 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 5,73e-159 Length: 2933
Score: 1632.50 Matches: 319
Percent Similarity: 98.46% Conservative: 0
Best Local Similarity: 98.46% Mismatches: 4
Query Match: 68.45% Indels: 3

DB:	2	Gaps:	0
US-10-019-341-3 (1-448) x AA233605 (1-2933)			
QY	126	ValHisLeuLeuGlyTyrSerLeuGlyAlaHisAlaAlaGlyIleAlaGlySerLeuThr	145
DB	1	GTCCATCTCTGGGATACAGCTTGGAGCCCATGCTGCTGGCATTTGAGGAAGTCTGACC	60
QY	146	AsnIysIysVal-AsnArgIleThrGlyLeuAspProAlaGlyProAsnPheGluIysAl	165
DB	61	AAATAAGAAAGTTCACAGAAATTACTGGCCCTCGATCCAGCTGGACCTTAACCTTTGAGTATGC	120
QY	165	gAluAlaProSerArgLeuSerProAspAspAlaAspPheValAspValLeuHisThrPh	185
DB	121	AGAAGCCCCGAGTCTTCTCTCTGATGATGACAGATTTTGTAGACGCTTTACACACATT	180
QY	185	eThrArgGlySerProGlyArgSerIleGlyIleGlnIysProValGlyHisValAspIl	205
DB	181	CACCAGAGGGTCCCTCGTGAAGCATTTGGAATCCAGAAACCATTTGGGCATGTTGACAT	240
QY	205	eTyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGluAlaIleArgValIl	225
DB	241	TTACCCGAATGGAGTACTTTTTCAGCCAGGATGTAACTTCGAGAGAGCTATCCGCGTGAT	300
QY	225	eAlaGluArgGlyLeuGlyAspValAspGlnLeuValLysCysSerHisGluArgSerIl	245
DB	301	TGCAGAGAGGACTTGGAGATGTGACAGCTAGTGAAGTGTCTCCACGAGCGCTCCAT	360
QY	245	eHisLeuPheIleAspSerLeuLeuAsnGluGluAsnProSerIysAlaTyrArgCysSe	265
DB	361	TCATCTCTTCATCGACTCTCTGTGAATGAAGAAATCCAGTAAGGCTACAGGTGCAG	420
QY	265	rSerIysGluAlaPheGluLysGlyLeuCysLeuSerCysArgLysAsnArgCysAsnAs	285
DB	421	TTCCAAGGAAGCCTTTGAGAAAGGCTCTGCTTGAGTTGTAGAAAGACCGCTGCAACAA	480
QY	285	nLeuGlyTyrGluIleAsnLysValArgAlaLysArgSerSerLysMetTyrLeuIysTh	305
DB	481	TCGGGCTATGAGTCAATCAATAAAGTCAGAGCCAAAGAACGAGCAAAATGACTGAAGAC	540
QY	305	rArgSerGlnMetProTyrIysValPheHisTyrGlnValLysIleHisPheSerGlyTh	325
DB	541	TCGTTCTCAGATGCCCTACAAAGTCTTCCATTACCAAGTAAGATTCATTTTCTGGGAC	600
QY	325	rGluSerGluThrHisThrAsnGlnAlaPheGluIleSerLeuTyrGlyThrValAlaGl	345
DB	601	TGAGAGTGAACCCATACCATCAGGCTTGAGAT--TCTCTGTATGGCACCGTGGCGGA	658
QY	345	uSerGluAsnIleProPheThrLeuProGluValSerThrAsnIysThrTyrSerPheLe	365
DB	659	GAGTGAGAACATCCCATTCCTCTGCTGAAGTTTCCACAAATAAGACCTTACTTCTCT	718
QY	365	uIleTyrThrGluValAspIleGlyGluLeuLeuMetLeuLysLeuLysIleLysSerAs	385
DB	719	AAATTTACACAGAGTAGATATTGGAGAACAC-CTCAAGTTGAGCTCAATGGAGAGTGA	777
QY	385	pSerTyrPheSerTrpSerAspTrpTrpSerProGlyPheAlaIleGlnIysIleAr	405
DB	778	TTTATATTAGTTAGTGTGACAGTGTGTGAGCAGTCCCGGCTTCGCCATTGAGAGATCAG	837
QY	405	gValLysAlaGlyGluThrGlnLysLysValIlePheCysSerArgGlnLysValSerHi	425
DB	838	AGTAAAGACGAGAGAGTCTCAGAAAAAAGGTGATCTTCTGTCTAGGGAGAAAGTCTTCA	897
QY	425	sLeuGlnIysGlyLysAlaProAlaValPheValLysCysHisAspLysSerLeuAsnLy	445
DB	898	TTTTCAGAAAGAAAGGACCTTGGGTATTGTGAAATGCCATGACAGTCTCTGTAATAA	957
QY	445	sLysSerGly	448
DB	958	GAGTTCAGGC	967

ABL91801	ABL91801 standard; DNA; 1503 BP.
XX	AC ABL91801;
XX	11-JUL-2002 (first entry)
XX	Human lipase endothelial (LIPG) isogene coding sequence.
XX	Human; ds, gene; single nucleotide polymorphism; SNP;
KW	lipase endothelial isogene; LIPG; drug screening; atherosclerosis;
KW	cardiovascular disorder; LIPG haplotyping; LIPG genotyping.
XX	Homo sapiens.
XX	Key
XX	CDS
FT	1. 1503
FT	/tag= a
FT	/product= "Human lipase endothelial (LIPG) protein"
FT	replace(12, A)
FT	allele
FT	/tag= b
FT	/standard_name= "Single nucleotide polymorphism"
FT	replace(160, T)
FT	allele
FT	/tag= c
FT	/standard_name= "Single nucleotide polymorphism"
FT	replace(332, T)
FT	allele
FT	/tag= d
FT	/standard_name= "Single nucleotide polymorphism"
FT	replace(831, G)
FT	allele
FT	/tag= e
FT	/standard_name= "Single nucleotide polymorphism"
XX	WO200216397-A2.
XX	28-FEB-2002.
XX	17-AUG-2001; 2001WO-US026639.
XX	25-AUG-2000; 2000US-0227825P.
XX	(GENA-) GENA155ANCE PHARM INC.
XX	Duda A, Kazeml A, Kliem SE, Messer C;
XX	WPI: 2002-292055/33.
XX	P-PSDB; AA014635.
XX	Novel genetic variants of Lipase, Endothelial isogenes, useful for
XX	improving efficiency and reliability in drug development for treating
XX	diseases associated with LIPG activity, e.g. atherosclerosis.
XX	Claim 25; Fig 2; 134pp; English.
XX	The invention comprises the DNA and amino acid sequence of the human
XX	lipase, endothelial (LIPG) isogene. Specifically, the invention relates
XX	to the discovery of 20 novel polymorphic sites within the LIPG gene. The
XX	LIPG coding sequence and protein are useful for screening drugs that can
XX	be used to treat atherosclerosis and other cardiovascular disorders. The
XX	LIPG coding sequence can also be used to haplotype and genotype the LIPG
XX	gene of an individual. The present DNA sequence represents the coding
XX	sequence of the human LIPG gene
XX	Sequence 1503 BP; 381 A; 398 C; 396 G; 328 T; 0 U; 0 Other;
XX	Alignment Scores:
XX	Pred. NO.: 2.34e-110 Length: 1503
XX	Score: 1161.00 Matches: 216
XX	Percent Similarity: 69.16% Conservative: 89
XX	Best Local Similarity: 48.98% Mismatches: 118
XX	Query Match: 48.68% Indels: 18
XX	DB: 6 Gaps: 6
XX	US-10-019-341-3 (1-448) x ABL91801 (1-1503)

QY	13	LysPheAlaLeuArgThrProGluAspThrAlaGluAspThrCysHisLeuIleProGly	32
Db	148	AGGTTTAACTCCGCACTCCAGGACCCAGCATGAAGATGCTACTCTCCGTGGC	207
QY	33	ValAlaGluSerValAlaThrCysHisPheAsnHisSerSerLysThrPheMetVal	52
Db	208	CACAGCCAGCCCTTAGAAGACTGCAGTTTCAACATGACACGTAAACCTTTTCATCATT	267
QY	53	HisGlyTyrThrValThrGlyMetTyrGluSerTyrValProLysLeuValAlaLeu	72
Db	268	CACGATGACATGACGCGTATCTTTGAAATCGGTGCACAACTCTGTGTGAGCCCTG	327
QY	73	TyrLysArgGluProAspSerAsnValIleValValAspTyrLeuSerArgAlaGlnGlu	92
Db	328	CACACAGAGAGAAAGAGGCCAATGTAGTTGTGGTTGACTGGCTCCCCCTGGCCCAACAG	387
QY	93	HisTyrProValSerAlaGlyTyrThrLysLeuValGlyGlnAspValAlaArgPheIle	112
Db	388	CTTTACACGGATGCGGTCAATATACACGGGTGTGGGACACAGCATTGCCAGGATGCTC	447
QY	113	AsnTyrMetGluGluGluPheAsnTyrProLeuAspAsnValHisLeuLeuGlyTyrSer	132
Db	448	GACTGCTCGAGAGAGACGACGATTTTCTCTCGGAATGTCCATCTGATGGCTACAGC	507
QY	133	LeuGlyAlaHisAlaGlyIleAlaGlySerLeuThrAsnLysLysValAsnArgIle	152
Db	508	CTCGAGGCGCAGTGGCCGGTATGCAGCAACTTCGTCAAAGAACGGTGGCCGAATC	567
QY	153	ThrGlyLeuAspProAlaGlyProAsnPheGluTyrAlaGluAlaProSerArgLeuSer	172
Db	568	ACAGTTTGTGATCTCGCCGGGCCCATGTTTGAAGCGGCGCACATCCACAGAGGCTCTCT	627
QY	173	ProAspAspAlaAspPheValAspValLeuHisThrPheThrArgGlySerProGlyArg	192
Db	628	COGAGCAGTGACAGATTGTGGATGTCTCCACACTACACGCGT---TCCTTGGCGTTG	684
QY	193	SerIleGlyIleGlnLysProValGlyHisValAspIleTyrProAsnGlyGlyThrPhe	212
Db	685	AGCATTGTATTTCAGATGCTGTGGCCACATTCGACATCTACCCCAATGGGGGTGACTTC	744
QY	213	GlnProGlyCysAsnIleGlyGluAlaIleArgValIleAlaGluArgGlyLeuGlyAsp	232
Db	745	CAGCCAGCGCTGGACTCAACGATGTCTTGGGATCAATTGCA-----TATGGAAACA	795
QY	233	ValAspGlnLeuValLysCysSerHisGluArgSerIleHisLeuPheIleAspSerLeu	252
Db	796	ATCACAGAGGTGGTAAATGTGACATGAGCGAGCCGTCCACCTCTTTGTGACTCTCTG	855
QY	253	LeuAsnGluGluAsnProSerLysAlaTyrArgCysSerSerLysGluAlaPheGluLys	272
Db	856	GTGAATCAGGACAGCCGAGTTTTCCTTCCAGTGCACTGCTCCCATCGCTTCAAAAG	915
QY	273	GlyLeuCysLeuSerCysArgLysAsnArgCysAsnAsnLeuGlyTyrGluIleAsnLys	292
Db	916	GGGATCTGTCTGAGCTCCGCAAGAACCGTTGTAATAGCATTTGGTCAATGCCAAGAAA	975
QY	293	ValArgAlaLysArgSerSerLysMetTyrLeuLysThrArgSerGlnMetProTyrLys	312
Db	976	ATGAGGAACACAGAGAACACCAATGTACTAAACCCGGCAGGCATGCCCTTTCAGA	1035
QY	313	ValPheHisTyrGlnValLysIleHisPheSerGlyThrGluSerGluThrHisThrAsn	332
Db	1036	GTTTACCATTTACAGATGAAATTCATGTCTTCAGTTACAGAACATGGAGAAATTGAG	1095
QY	333	GlnAlaPheGluIleSerLeuTyrGlyThrValAlaGluSerGluAsnIleProPheThr	352
Db	1096	CCACCTTTTACGTGTCACCTTTATGACCTAATATGCAGATTCCAGACTCTGCCACTGGAA	1155
QY	353	LeuProGlu---ValSerThrAsnLysThrTyrSerPheIleIleTyrThrGluValAsp	371
Db	1156	ATAGTGGCGGATCAGCAGNATGCCAACACCTTCTGGTCTACACCGAGAGAC	1215

Qy	372	IleGlyGluLeuLeuMetLeuLysLeuLysTyrLysSerAspSerTyrPheSerTrpSer	391
Db	1216	TTGGGAGACCTCTTGAAGATCCAGTCACTCGGAGGGGGCCCTCTCAG---	1272
Qy	392	AspTrpTrpSer-----SerProGly-----Phe	399
Db	1273	AACCTGTGAAGAGAGTTTCGCAGTACCTGTCTCAACCCCGCAACCCCGGACGGAGCTG	1332
Qy	400	AlaIleGlnLysIleArgValLysAlaGlyGluThrGlnLysLysValIlePheCysSer	419
Db	1333	AATATCAGCGGCATCCGGGTGAAGTCTGGGAAACCCAGCGGAACTGACATTTGTACA	1392
Qy	420	ArgGluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHis	439
Db	1393	GAAGACCTCTGAGAACACACCCAGCATATCCCCAGCGCGGAGCTCTGGTTTCGCAAGTGTGCG	1452
Qy	440	Asp	440
Db	1453	GAT	1455
RESULT 15			
AAx85838			
ID	AAx85838 standard; cDNA; 1755 BP.		
AC	AAx85838;		
XX			
DT	09-SEP-1999 (first entry)		
XX			
DE	cDNA encoding human endothelial cell lipase.		
XX			
KW	Endothelial lipase; hypertriglyceridemia; hypercholesterolemia; cancer;		
KW	de nova imaging; endothelial cell; tumour; vascular disorder; lipidemia;		
KW	diabetes; obesity; restenosis; cancer; ss.		
XX			
OS	Homo sapiens.		
XX			
PN	WO9932611-A1.		
XX			
PD	01-JUL-1999.		
XX			
PF	21-DEC-1998; 98WO-US027335.		
XX			
PR	19-DEC-1997; 97US-0068336P.		
XX			
PA	(PROG-) PROGENITOR INC.		
PA	(UYVA-) UNIV VANDERBILT.		
XX			
PI	Hirata K, Quertermous T, Cioffi JA, Zupancic T;		
XX			
DR	WPI; 1999-418920/35.		
DR	P-PSDB; AAY23759.		
XX			
PT	An endothelial lipase and related polynucleotides, useful in diagnosis		
PT	and treatment of vascular disorders, lipidemia and diabetes.		
XX			
PS	Claim 2; Fig 1A-C; 78pp; English.		

XX The present sequence encodes an endothelial lipase. Detecting the
CC decreased or increased expression of a human endothelial lipase gene can
CC be used to diagnose hypertriglyceridemia and hypercholesterolemia,
CC respectively. The lipase itself can be used to treat these conditions.
CC Additionally, decreasing the expression of the lipase can be used to
CC treat cancer. The antibodies may be used as a non-invasive diagnostic
CC tool for imaging de novo endothelial cells in tumours and metastases.
CC Hybrid antibodies may be used to specifically eliminate endothelial
CC lipase expressing blood vessels in tumours. The endothelial lipase can
CC also be used in diagnosis and treatment of vascular disorders, lipidemia,
CC diabetes and associated complications, obesity, restenosis and cancer
XX
SQ Sequence 1755 BP; 419 A; 475 C; 473 G; 388 T; 0 U; 0 Other

Alignment Scores:
Pred. No.:

Score: 1161.00 Matches: 216
 Percent Similarity: 69.16% Conservative: 89
 Best Local Similarity: 48.98% Mismatches: 118
 Query Match: 48.68% Indels: 18
 DB: 2 Gaps: 6

US-10-019-341-3 (1-448) x AAX85838 (1-1755)

1348 CCCACCTTTTACGTCACCCCTTTATGACACTAATGACAGATTCCAGACTCTGCCACTGGAA 1407
 353 LeuProGlu---ValSerThrAsnLysThrTyrSerPheLeuIleTyrThrGluValAsp 371
 1408 ATAGTGGAGCGGATCGAGCAGATGCCACCAACCTTCTGCTCTACACCGAGGAGGAC 1467
 372 IleGlyGluLeuMetLeuLysLeuLysLeuLysSerAspSerTyrPheSerTyrSer 391
 1468 TTGGAGACCTCTTGAAGATCCAGCTCACCTGGGAGGGGGCTCTCAG---TCTTGGTAC 1524
 392 AspTrpTrpSer-----SerProGly-----Phe 399
 1525 AACCTGTGGAAGGAGTTTCGACGCTACCTGTCTCAACCCGCAACCCCGGACGGAGCTG 1584
 400 AlaIleGlnLysIleArgValLysAlaGlyGluThrGlnLysLysValIlePheCysSer 419
 1585 AATATCAGGGCGCATCCGGGTGAAGTCTGGGGGAACCCAGCGGAACCTGACATTTGTACA 1644
 420 ArgGluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHis 439
 1645 GAAGACCTGAGAACACACCGACATATCCCGAGCGGGAGCTCTGTTTCGCAAGTGTGG 1704
 440 Asp 440
 1705 GAT 1707

Search completed: October 24, 2004, 18:17:59
 Job time : 718 secs

1161.00 Matches: 216
 69.16% Conservative: 89
 48.98% Mismatches: 118
 48.68% Indels: 18
 2 Gaps: 6

US-10-019-341-3 (1-448) x AAX85838 (1-1755)

13 LysPheAlaLeuArgThrProGluAspThrAlaGluAspThrCysHisLeuIleProGly 32
 400 AGGTTTAACTCCGACCTCCAGAGACCAGAGCATGACGATGCTACCTCTCGTCCGC 459
 33 ValAlaGluSerValAlaThrCysHisPheAsnHisSerSerLysThrPheMetValIle 52
 460 CACAGCCAGCCCTTAGAGAGCTGCAGTTTCAACATGACAGCTAAACCTTTTTCATCATT 519
 53 HisGlyTrpThrValThrGlyMetTyrGluSerTrpValProLysLeuValAlaAlaLeu 72
 520 CACGGATGGACGATGAGCGGTATCTTTGAAGACTGGCTGCACAACTCTGTCAGCCCTG 579
 73 TyrLysArgGluProAspSerAsnValIleValValAspTrpLeuSerArgAlaGlnGlu 92
 580 CACACAGAGAGAAAGACGCCAATGTAGTTGTGTTGACTGGCTCCCGCTGGCCACGAG 639
 93 HisTyrProValSerAlaGlyTyrThrLysLeuValGlyGlnAspValAlaArgPheIle 112
 640 CTTTACACGGATGCGGTCAATAATACCGGGTGTGGGACACAGCATTTGCCAGGATGCTC 699
 113 AsnTrpMetGluGluGluPheAsnTyrProLeuAspAsnValHisLeuLeuGlyTyrSer 132
 700 GACTGGCTGCAGGAGAGACGATTTTCTCTCGGGAATGTCCACTTGTATCGGCTACAGC 759
 133 LeuGlyAlaHisAlaAlaGlyIleAlaGlySerLeuThrAsnLysLysValAsnArgIle 152
 760 CTCGGAGCCACGTCGCGCGGTATGCGGCACTTCGTGAAGGACGCTGGCGGGAATC 819
 153 ThrGlyLeuAspProAlaGlyProAsnPheGluTyrAlaGluAlaProSerArgLeuSer 172
 820 ACAGGTTTGGATCTCGCGGCGCCATGTTTGAAGGGCGGACATCCACAGAGGCTCTCT 879
 173 ProAspAlaAspPheValAspValLeuHisThrPheThrArgGlySerProGlyArg 192
 880 CCGGACGATGCAGATTTTGGATGCTCCACACCTACACGCT---TCTTCGGCTTG 936
 193 SerIleGlyIleGlnLysProValGlyHisValAspIleTyrProAsnGlyGlyThrPhe 212
 937 AGCATTTGGTATTGATGCTGCTGGGCCACATTGACATCTACCCCAATGGGGGTGACTTC 996
 213 GlnProGlyCysAsnIleGlyGluAlaIleArgValIleAlaGluArgGlyLeuGlyAsp 232
 997 CAGCCAGGCTGTGGACTCAACGATGCTTGGGATCAATTGCA-----TATGGAACA 1047
 233 ValAspGlnLeuValLysCysSerHisGluArgSerIleHisLeuPheIleAspSerLeu 252
 1048 ATCAGAGAGGTGTAATAATGACATGAGCGGCGCTCCACCTCTTTGTGACTCTCTG 1107
 253 LeuAsnGluGluAsnProSerLysAlaTyrArgCysSerSerLysGluAlaPheGluLys 272
 1108 GTGATCTGTCTGAGTCCGCAAGACCGTTTGTGATGATGCTTCCAGTGCCTGACTCCAAATCGCTTCAAAAAG 1167
 273 GlyLeuCysLeuSerCysArgLysAsnArgCysAsnAsnLeuGlyTyrGluIleAsnLys 292
 1168 GGGATCTGTCTGAGTCCGCAAGACCGTTTGTGATGATGCTTCCAGTGCCTGACTCCAAATCGCTTCAAAAAG 1227
 293 ValArgAlaLysArgSerSerLysMetTyrLeuLysThrArgSerGlnMetProTyrLys 312
 1228 ATGAGGAAACAAGAGAACAGCAAAATGTACTTAAACCCCGGCGAGCATGCTCTTTCAGA 1287
 313 ValPheHisTyrGlnValLysIleHisPheSerGlyThrGluSerGluThrHisThrAsn 332
 1288 GTTTACCATTTATCAGATGAAATCCATGCTTCAAGAACATCGGAGAAATTGAG 1347
 333 GlnAlaPheGluIleSerLeuTyrGlyThrValAlaGluSerGluAsnIleProPheThr 352

GenCore version 5.1.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 24, 2004, 18:18:05 ; Search time 125 Seconds
(without alignments)

2547.467 Million cell updates/sec

Title: US-10-019-341-3

Perfect score: 2385

Sequence: 1 ADOORDFIDIESKALRTEP.....GKAPAVFKCHDKSLNKSG 448

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Issued Patents NA -QWMT=fascap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human4.0.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:
5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq:
6: /cgn2_6/ptodata/1/ina/backfiles.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	SUMMARIES			Description
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3	928	38.9	1035	US-08-985-492-9
4	928	38.9	1065	US-08-985-492-5
5	928	38.9	1382	US-08-985-492-3
6	928	38.9	1510	US-10-140-002-399
7	634	26.6	9734	US-09-347-114A-80
8	461.5	19.4	1401	US-09-411-132A-2
9	461.5	19.4	2352	US-09-411-132A-1
10	451.5	18.9	1206	US-09-513-999C-79
11	414	17.4	231	US-08-905-124-4
12	363	15.2	1889	US-09-799-451-90
13	328.5	13.8	1050	US-08-180-209B-16
14	328.5	13.8	1050	US-08-385-745-16
15	328.5	13.8	1050	US-08-485-388-16
16	328.5	13.8	1050	US-08-474-853-16
17	328.5	13.8	1050	US-09-166-205B-16
18	328.5	13.8	1050	PCT-US94-02629-16
19	327	13.7	3877	US-09-347-114A-81
20	327	13.7	3877	US-09-054-272-54
21	320.5	13.4	856	US-09-270-767-11560
22	306.5	12.9	1048	US-09-166-205B-63
23	306.5	12.9	1048	US-09-806-658-1
24	304	12.7	761	US-09-270-767-14310
25	294	12.3	1341	US-08-180-209B-26
26	294	12.3	1341	US-08-385-745-26
27	294	12.3	1341	US-08-485-388-26
28	294	12.3	1341	US-08-474-853-26
29	294	12.3	1341	US-09-166-205B-26
30	294	12.3	1341	PCT-US94-02629-26
31	282.5	11.8	1168	US-09-270-767-662
32	282.5	11.8	1168	US-09-270-767-15944
33	276.5	11.6	579	US-09-270-767-1889
34	276.5	11.6	579	US-09-270-767-17171
35	259	10.9	430	US-09-270-767-16345
36	259	10.9	430	US-09-270-767-16345
37	236	9.9	225	US-08-985-492-11
38	236	9.9	1398	US-09-270-767-11578
39	192	8.1	558	US-09-270-767-27181
40	189	7.9	1889	US-09-799-451-90
41	173	7.3	367	US-08-985-492-1
42	169.5	7.1	8442	US-09-272-032-6
43	146.5	6.1	570	US-09-513-999C-80
44	123	5.2	220	US-09-270-767-27160
45	115.5	4.8	400	US-09-513-999C-81

ALIGNMENTS

RESULT 1

US-09-054-272-39
; Sequence 39, Application US/09054272
; Patent No. 6692909
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Daley, George Q.
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Rozen, Steven G.
; TITLE OF INVENTION: CODING SEQUENCE POLYMORPHISMS
; TITLE OF INVENTION: IN VASCULAR PATHOLOGY GENES
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/054,272
; FILING DATE: 01-APR-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: WHI98-05

Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 81, Appl
Sequence 54, Appl
Sequence 11560, A
Sequence 63, Appl
Sequence 1, Appli
Sequence 14310, A
Sequence 26, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 662, App
Sequence 15944, A
Sequence 1889, Ap
Sequence 17171, A
Sequence 1063, Ap
Sequence 16345, A
Sequence 11, Appl
Sequence 11578, A
Sequence 27181, A
Sequence 90, Appl
Sequence 1, Appl
Sequence 6, Appli
Sequence 80, Appl
Sequence 27160, A
Sequence 81, Appl

Mon Oct 25 15:42:53 2004

TELECOMMUNICATION INFORMATION:

TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
TELEX:

INFORMATION FOR SEQ ID NO: 39:

SEQUENCE CHARACTERISTICS:

LENGTH: 3549 base pairs
TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Genomic DNA

FEATURE:

NAME/KEY: Coding Sequence

LOCATION: 175...1599

OTHER INFORMATION:

US-09-054-272-39

Alignment Scores:

Pred. No.:	1.68e-277	Length:	3549
Score:	2385.00	Matches:	448
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-019-341-3 (1-448) x US-09-054-272-39 (1-3549)

QY	1	AlaaspGlnArgAspPheIleAspIleGluSerLysPheAlaLeuArgThrProGlu	20
DB	256	GCCGACCAAGAGATTTATCGACATCGAAGTAATTTGCCCTAAGGACCCCTGAA	315
QY	21	AspThrAlaGluAspThrCysHisLeuIleProGlyValAlaGluSerValAlaThrCys	40
DB	316	GACACAGCTGAGGACATTGCCACCTATCCCGGAGTAGCAGAGTCCGTGGCTACCTGT	375
QY	41	HisPheAsnHisSerSerLysThrPheMetValIleHisGlyThrValThrGlyMet	60
DB	376	CATTTCAATACACAGCAGCAAACTTCATGGTGATCCATGGCTGGACGTTAACAGGATG	435
QY	61	TyrGluSerTyrValProLysLeuValAlaAlaLeuTyrLysArgGluProAspSerAsn	80
DB	436	TATGAGATGGTGCCAAACTTTGGCGCCCTGTACAGAGAGAACACAGACTCCAAT	495
QY	81	ValIleValValAspThrLeuSerArgAlaGlnGluHisTyrProValSerAlaGlyTyr	100
DB	496	GTCAATTTGGTGACTGGCTGCACGGGCTCAGGAGCATTACCCAGTGTCCCGGGCTAC	555
QY	101	ThrLysLeuValGlyGlnAspValAlaArgPheIleAsnTyrMetGluGluGluPheAsn	120
DB	556	ACCAAACTGGTGGGACAGGATGGCCCGGTTTATCAACTGGATGGAGGAGGTTTAAC	615
QY	121	TyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeuGlyAlaHisAlaAlaGlyIle	140
DB	616	TACCCCTGTGACAAATGTCATCTCTGGGATACAGCCTTGGAGCCCATGCTGGGCAAT	675
QY	141	AlaGlySerLeuThrAsnLysLysValAsnArgIleThrGlyLeuAspProAlaGlyPro	160
DB	676	GCAGGAAGTCTGACCAATAGAAAGTCAACAGAAATTAATGGCTCGATCCAGCTGGACCT	735
QY	161	AspPheGluTyrAlaGluAlaProSerArgLeuSerProAspAspAlaAspPheValAsp	180
DB	736	AACTTTGAGTATGAGAAGCCCGAGTCGTCTTCTCCTGATGATGAGATTTGTAGAC	795
QY	181	ValLeuHisThrPheThrArgGlySerProGlyArgSerIleGlyIleGlnLysProVal	200
DB	796	GTCTTACACATTCACAGAGGGTCCCTGGTGGAGGATTTGGAATCCAGAAACCACTT	855
QY	201	GlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGlu	220
DB	856	GGGCATGTGACATTTACCGAATGGAGGTACTTTTCAGCCAGGATGTAACATTTGGAGAA	915
QY	221	AlaIleArgValIleAlaGluArgGlyLeuGlyAspValAspGlnLeuValLysCysSer	240

DB	916	GCTATCCGCGTGATTGACAGAGAGAGACTTGGAGATGTGGACCGAGCTAGTGAAGTGTCC	975
QY	241	HisGluArgSerIleHisLeuPheIleAspSerLeuLeuAsnGluGluAsnProSerLys	260
DB	976	CACGAGCGCTCCATTCATCTCTTCATCGACTCTCTGTTGAATGAAGAAATCCAAAGTAAG	1035
QY	261	AlaTyrArgCysSerSerLysGluAlaPheGluLysGlyLeuCysLeuSerCysArgLys	280
DB	1036	GCCTACAGGTGCAGTTCCAAGGAAGCCTTTGAGAAAGGGCTCTCTTGAGTTGTAGAAAG	1095
QY	281	AsnArgCysAsnAsnLeuGlyTyrGluIleAsnLysValArgAlaLysArgSerSerLys	300
DB	1096	AACCGCTGCCAATCTGGGCTATGAGATCAATAAAGTCAGAGCCAAAGAGACGACAA	1155
QY	301	MetTyrLeuLysThrArgSerGlnMetProTyrLysValPheHisTyrGlnValLysIle	320
DB	1156	ATGTACCTGAAGACTCGTTCTCAGATGCCCTACAAAGTCTTCCATTTACCAAGTAAAGATT	1215
QY	321	HisPheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGluIleSerLeuTyr	340
DB	1216	CATTTTCTGGGACTGAGAGTGAAACCCATACCAATCAGGCTTTGAGATTCTCTGTAT	1275
QY	341	GlyThrValAlaGluSerGluAsnIleProPheThrLeuProGluValSerThrAsnLys	360
DB	1276	GGCACCGTGGCGGAGAGTGAAGACATCCCATTCATCTGCTGAGATTCCACAATAAG	1335
QY	361	ThrTyrSerPheLeuIleTyrThrGluValAspIleGlyGluLeuLeuMetLeuLysLeu	380
DB	1336	ACCTACTCTCTTCTTAATTTACACAGAGGTAGATATTGAGAACTACTCATGTGAGCTC	1395
QY	381	LysTrpLysSerAspSerTyrPheSerTrpSerAspTrpTrpSerSerProGlyPheAla	400
DB	1396	AAATGGAAGAGTGATTCATCTTACTAGCTGGTCAGACTGGTGAGCAGTCCCGCTTCGCC	1455
QY	401	IleGlnLysIleArgValLysAlaGlyGluThrGlnLysLysValIlePheCysSerArg	420
DB	1456	ATTCAAGATCAGAGTAAAGCAGGAGAGACTCAGAAAAGGTGATCTCTGTTCTAGG	1515
QY	421	GluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHisAsp	440
DB	1516	GAGAAAGTGTCTCATTTTGCAGAAAGGAAGGACCTCGCGTATTTGTGAATGCCATGAC	1575
QY	441	LysSerLeuAsnLysLysSerGly	448
DB	1576	AAGTCTCTGAATAAGAAGTCAGGC	1599

RESULT 2

US-08-985-492-7

Sequence 7, Application US/08985492

Patent No. 6395530

GENERAL INFORMATION:

APPLICANT: Jaye, Michael C.

APPLICANT: Doan, Kim-Anh T.

APPLICANT: Krawiec, John A.

APPLICANT: Lynch, Kevin J.

APPLICANT: Amin, Dilip V.

APPLICANT: South, Victoria J.

TITLE OF INVENTION: LG POLYPEPTIDES OF THE TRIACYLGLYCEROL

TITLE OF INVENTION: LIPASE FAMILY AND COMPOSITIONS AND METHODS FOR THEIR USE

NUMBER OF INVENTION: IN ENZYMIC HYDROLYSIS, AND PROTEIN AND GENE THERAPIES

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESS: Rhone-Poulenc Rorer Inc.

STREET: 500 Arcola Rd. 3043

CITY: Collegeville

STATE: PA

COUNTRY: USA

ZIP: 19426

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30


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; LOCATION: 1..1065
US-08-985-492-5
Alignment Scores:
Pred. No.: 4,12e-102 Length: 1065
Score: 928.00 Matches: 165
Percent Similarity: 75.33% Conservative: 61
Best Local Similarity: 55.00% Mismatches: 70
Query Match: 38.91% Indels: 4
DB: 3 Gaps: 2

US-10-019-341-3 (1-448) x US-08-985-492-5 (1-1065)
QY 13 LysPheAlaLeuArgThrProGluAspThrAlaGluAspThrCysHisLeuIleProGly 32
Db 148 AGGTTTAACTCCGACCTCCCAAGGACCCAGAGCATGAAGATGCTTCTCCGTCGCGC 207
QY 33 ValAlaGluSerValAlaThrCysHisPheAsnHisSerSerIysThrPheMetValIle 52
Db 208 CACAGCCAGCCCTTAAAGACTGCAAGTTCACATGACAGCTAAACCTTTTCATCAT 267
QY 53 HisGlyTyrThrValThrGlyMetTyrGluSerTyrValProIysLeuValAlaLeu 72
Db 268 CACGATGACGATGAGCGTATCTTTGAAACTGGCTGCACAACTCGTGTGAGCCCTG 327
QY 73 TyrLysArgGluProAspSerAsnValIleValAspTyrLeuSerArgAlaGlnGlu 92
Db 328 CACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 387
QY 93 HisTyrProValSerAlaGlyTyrThrLysLeuValGlyGlnAspValAlaArgPheIle 112
Db 388 CTTTACAGGATGGGTGATTAATACAGGAGTGTGGGACAGCATTTGCCAGGATGCTC 447
QY 113 AsnTyrMetGluGluGluPheAsnTyrProLeuAspAsnValHisLeuGlyTyrSer 132
Db 448 GACTGGCTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 507
QY 133 LeuGlyAlaHisAlaAlaGlyIleAlaGlySerLeuThrAsnLysLysValAsnArgIle 152
Db 508 CTCGAGCGCAGCTGGCGGCTATGACGAGCACTTCGTAAGAGAGAGAGAGAGAGAG 567
QY 153 ThrGlyLeuAspProAlaGlyProAsnPheGluTyrAlaGluAlaProSerArgLeuSer 172
Db 568 ACAGTTTGGATCTCGCGGCGCCATGTTGAAGGCGCGGACATCCACAGAGAGCTCTCT 627
QY 173 ProAspAlaAspPheValAspValLeuHisThrArgGlySerProGlyArg 192
Db 628 CCGGACCATGAGATTTTGGATGCTCTCCACACCTTACAGCGGT---TCCTCGGCTTG 684
QY 193 SerIleGlyLeuGlnLysProValGlyHisValAspIleTyrProAsnGlyGlyThrPhe 212
Db 685 AGCATTTGGTATTCAGATGCTGTTGGGCGCCATTCACATTCACCCCAATGGGGTGACTTC 744
QY 213 GlnProGlyCysAsnIleGlyGluAlaIleArgValIleAlaGluArgGlyLeuGlyAsp 232
Db 745 CAGCCAGGCTGTGAGCTCAACGATGCTTGGGATCAATTGCA-----TATGGAACA 795
QY 233 ValAspGlnLeuValLysCysSerHisGluArgSerIleHisLeuPheIleAspSerLeu 252
Db 796 ATCAGAGAGGTGTAAATGTGAGATGAGCGAGCGGTCACCTCTTTGTGACTCTCTG 855
QY 253 LeuAsnGluGluAsnProSerIysAlaTyrArgCysSerSerLysGluAlaPheGluLys 272
Db 856 GTGAATCAGACAGCAAGCGAGTTTGTCTCCAGTGCACCTGACCTCCCAATCGCTTCAAAAG 915
QY 273 GlyLeuCysLeuSerCysArgLysAsnArgCysAsnAsnLeuGlyTyrGluIleAsnLys 292
Db 916 GGGATCTGTGAGCTGCGCGCAAGACCGTGTAAATAGCATTTGGCTTACATGCCAAGAAA 975
QY 293 ValArgAlaLysArgSerSerLysMetTyrLeuLysThrArgSerGlnMetProTyrLys 312
Db 976 ATCAGGACACAGAGGAGACGAAATGTATCTTAAATAACCCGCGGAGGATGCTTTCAGA 1035
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RESULT 5
US-08-985-492-3
; Sequence 3, Application US/08985492
; Patent No. 6395530
; GENERAL INFORMATION:
; APPLICANT: Jaye, Michael C.
; APPLICANT: Doan, Kim-Anh T.
; APPLICANT: Krawiec, John A.
; APPLICANT: Lynch, Kevin J.
; APPLICANT: Amin, Dilip V.
; APPLICANT: South, Victoria J.
; TITLE OF INVENTION: ILG POLYPEPTIDES OF THE TRIACYLGLYCEROL
; TITLE OF INVENTION: LIPASE FAMILY, AND COMPOSITIONS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Rd. 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,492
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Fehlnher Ph.D., Paul F.
; REGISTRATION NUMBER: 35,135
; REFERENCE/DOCKET NUMBER: A2582-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610)454-3839
; TELEFAX: (610)454-3808
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1382 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: Double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 312..1370
; US-08-985-492-3
Alignment Scores:
Pred. No.: 6,45e-102 Length: 1382
Score: 928.00 Matches: 165
Percent Similarity: 75.33% Conservative: 61
Best Local Similarity: 55.00% Mismatches: 70
Query Match: 38.91% Indels: 4
DB: 3 Gaps: 2
US-10-019-341-3 (1-448) x US-08-985-492-3 (1-1382)
QY 13 LysPheAlaLeuArgThrProGluAspThrAlaGluAspThrCysHisLeuIleProGly 32
Db 459 AGGTTTAACTCCGACCTCCCAAGGACCCAGAGCATGAAGATGCTTCTCCGTCGCGC 518
QY 33 ValAlaGluSerValAlaThrCysHisPheAsnHisSerSerIysThrPheMetValIle 52
Db 519 CACAGCCAGCCCTTAAAGACTGCAAGTTCACATGACAGCTAAACCTTTTCATCAT 578
QY 53 HisGlyTyrThrValThrGlyMetTyrGluSerTyrValProIysLeuValAlaLeu 72
Db 579 CACGATGAGCATGAGCGGTATCTTTGAAATACTGGCTGCACAACTCGTGTGAGCCCTG 638
QY 73 TyrLysArgGluProAspSerAsnValIleValAspThrLysArgAlaGlnGlu 92

Db 1138 GGGATCTGCTGAGCTGCCGCAAGAACCGTTGTAATAGCATTTGGCTACAATGCCAAGAA 1197
Qy 293 ValArgAlaLysArgSerLysMetTyrLeuLysThrArgSerGlnMetProTyrLys 312
Db 1198 ATGAGGACAGAGGACAGCAAAATGCTCTAAACCCCGGCGAGGCATGCGCTTTCAGA 1257

RESULT 7

US-09-347-114A-80
; Sequence 80, Application US/09347114A
; Patent No. 6297014
; GENERAL INFORMATION:
; APPLICANT: Kent D. Taylor (Inventor)
; APPLICANT: Karen T. Scheuner (Inventor)
; APPLICANT: Jerome I. Rotter (Inventor)
; APPLICANT: Huiying Yang (Inventor)
; TITLE OF INVENTION: Genetic Test to Determine
; FILE OF INVENTION: No. 6297014-responsiveness to Statin Drug Treatment
; FILE REFERENCE: P07 41878
; CURRENT APPLICATION NUMBER: US/09/347,114A
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 9734
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-347-114A-80

Alignment Scores:
Pred. No.: 6,92e-65 Length: 9734
Score: 634.00 Matches: 196
Percent Similarity: 21.27% Conservative: 2
Best Local Similarity: 21.05% Mismatches: 4
Query Match: 26.58% Indels: 730
DB: 3 Gaps: 2

US-10-019-341-3 (1-448) x US-09-347-114A-80 (1-9734)

Qy 111 PheIleAsnTrpMetGluGluGluPheAsnTyrProLeuAspAsnValHisLeuLeuGly 130
Db 122 TTTCTTTTCTCCAAAGAGAGAGATTAACTACCTCTGGCAATGTCTCTTGGA 181
Qy 131 TyrSerLeuGlyAlaHisAlaAlaGlyLeuAlaGlySerLeuThrAsnLysValAsn 150
Db 182 TACAGCCTTGGAGCCCATGCTGCTGGCATTGCGAGAGTCTGACCAATAGAAAGTCAAC 241
Qy 151 ArgIleThrGlyLeu----- 155
Db 242 AGAATTACTGGTAA-GAAAGCAATTCGTTGGTCTTATCATAGAGGTGAAAGACTGTC 300
Qy 155 ----- 155
Db 301 ATTCTGAGAGAGATCAGAACAAATTTGTTAAATACCCACATGTGTGTTCTTCCCG 360
Qy 155 ----- 155
Db 361 GAGACATGACCAGACTTGATATCTCATTTAGGGCTCTTTATTAGGATAGAAAAA 420
Qy 155 ----- 155
Db 421 CACAGAGGCTCTCACTGGCTTACTATCCACTGGCAATAGCACAGAAATAAAGCATTA 480
Qy 155 ----- 155
Db 481 CACAAATGCTCGAGATTCTCTGGGAAGCCTGTTTCTCCCACTCTCAGCTCTGTGT 540
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Db 541 TTAGTAGTGTAAATGCACATCAGTACTAGGAGAAAGAGAGACCAATTCAGAGGCC 600
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Db 601 ACTTCGAAAGAGACCGCTCATCTAGGCAAGGTGTGGCATATACACAGAGAGAAAGAAC 660

Qy 155 ----- 155
Db 661 CACCACCTGTTTATACATCTTCTCGACATATTTCAGAAATAATCTACAAAAGAAATCCAGC 720
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Db 721 CATCTGAGTGGAAATTGCTGCATAAGGCTAGTTTAAAGAGACTCAAAATTCATTTTAGAAG 780
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Db 781 GAGCAAGCCTCTCTTTTATGTCTCTCTAAAGTAAAGATACCATGACTGTAGATAGAGCT 840
Qy 155 ----- 155
Db 841 AATAAGAAATCTAAATAGTGCAGAGTGCATTCAAATGATGAGCAGTGCATGCGAATGTCA 900
Qy 156 ----- AspPro 157
Db 901 TACGAATGGAAATTTTACAAATCTGTGTTCTCTGCTTTTTCCTTTTAAAGGCCTCGATCCA 960
Qy 158 AlaGlyProAsnPheGluTyrAlaGluAlaProSerArgLeuSerProAspAspAlaAsp 177
Db 961 GCTGGACCTAACCTTTGAGTATGCAGAGCCCGAGTCTGTTCTCTCTGATGATGCAGAT 1020
Qy 178 PheValAspValLeuHisThrPheThrArgGlySerProGlyArgSerIleGlyIleGln 197
Db 1021 TTTGTAGAGCTTTACACACATTCACAGAGGCTCCCTGGTCGAGCAATTCGAATCCAG 1080
Qy 198 LysProValGlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGlyCysAsn 217
Db 1081 AAACCAAGTTGGGCATGTTGACATTTACCCGAATGAGGACTTTTCCGCCAGGATGTAAC 1140
Qy 218 IleGlyGluAlaIleArgValIleAlaGluArgGlyLeuGly----- 231
Db 1141 ATTGGAGAGCTATCCGCGTGAITTCAGAGAGGACTTGGAGGTAATATTATTATTAGAA 1200
Qy 231 ----- 231
Db 1201 GCGAATTAATGTGACTCTTATCCTTAACCTTATTGACCAATGTCTCTACTAGTAGCT 1260
Qy 231 ----- 231
Db 1261 TCAAAGTATGTAGTTTTCATATACACATTTGGCCAAATTAATGTTCTGAAGAAATCTGCA 1320
Qy 231 ----- 231
Db 1321 ATGTTACAGATGACCCTTTAGAGCCAGGCAGACAGCCATTTTATCTTTTATTACTATA 1380
Qy 231 ----- 231
Db 1381 CTGTAGGCTACATGAGCAGTGCATTTACAGTAGCAAGAAAAGGTTAGATGTTTACTAGAC 1440
Qy 231 ----- 231
Db 1441 AGGAAGACTCCAGTCACTCAATAATGGCATCATATAAATGCTATCTGGCCACATGTTGTC 1500
Qy 231 ----- 231
Db 1501 ATACCTTGAATGTAGTGCAGAACCCAAATGGAAAGATTTTAGATGTTTACTGGAACAGA 1560
Qy 231 ----- 231
Db 1561 TGTTAATTAGCATAAATCTTCCAAATGTTTCAGAACATAATGTAGCTTAATGTTTACT 1620
Qy 231 ----- 231
Db 1621 TTAATAATGTAGCTGTGTAAATTTATGATTTTGTGTTGTTTGTGATAGTAGAG 1680
Qy 231 ----- 231
Db 1681 TCTTATTCTATTGGCCCAAGCTGGGGTGCAGTCAACAATCACAGGAGCTTGCAATGTTGC 1740

QY 231 ----- 231
Db 1741 CCAGGCTGCTCAAACTCCTGGCCCTCAAGTGTCTCTCTGCTCAGCCTCCCAAGATTC 1800
QY 231 ----- 231
Db 1801 TGGGATTGCAGCTGTGAGCCACACGCCAGCTTTACGATTATTTTAAAGGCCCTTGC 1860
QY 231 ----- 231
Db 1861 ATACTTTATAGACATTGGGACCTACCTAGGATATCTCTGTTATTTTGTGCAGCTAATAG 1920
QY 231 ----- 231
Db 1921 AACTTAGAGCATATTGTACTATTTTCGATTGTCTTAAACTTTACAAGGAATCAATCT 1980
QY 231 ----- 231
Db 1981 TATGCCATTGCTGATTATTTCTATGTTCAATTAAGAGAGTGTAGTAGGGCAGA 2040
QY 231 ----- 231
Db 2041 ACCCTCAATTGTACATAATATCAATGATAAATAACAATTCATTTAAACAATTACCCTCTTA 2100
QY 231 ----- 231
Db 2101 AGATGTGTTTCTAGAAATACAAATGTCTCTAATTACAGTTTCCAACTTTACAATTG 2160
QY 231 ----- 231
Db 2161 GGCCTGAACACATTTTAAGTTGAGAAGCACGTGATGTTTGACCTTAAACTTTTGACA 2220
QY 231 ----- 231
Db 2221 TTATGATGGTTTGGGGTATTAGTGCAATTTTGACTTACAGTATTTTGACTTATGAA 2280
QY 231 ----- 231
Db 2281 GAATTATTGTAAGCAAGGGCAGGTATATGTTTCTAGAAGCACCTAGAAGTGTAGAC 2340
QY 231 ----- 231
Db 2341 ACTTTCAATGTAAGAGAGATGAGATAAACAAGGAATACACACTCCACCTTGGAGGCT 2400
QY 231 ----- 231
Db 2401 TATTACAGCTTCATAAACATCTATATAATAAAGAACACAAAAGTCAAAAATTCCTCTG 2460
QY 231 ----- 231
Db 2461 TGAACCTTGCAACTTTCACCTCTTTGAAGGTGGGTGGCGCGCTACCACCAAGAAATATCTCC 2520
QY 231 ----- 231
Db 2521 TGAATAGGCGCTACAAATCATAAATGCAAGGACTATATCCTTGGGTGATTCTACTTAA 2580
QY 231 ----- 231
Db 2581 CACCACATCTCACCTATTTTAGACATGCCAAATGAAACACTTTTGTGAATTTTGTGCCGA 2640
QY 232 ----- 231
Db 2641 GATACAACTCTGGTGTCTCTTTTTCACAGATGTGGCAGCTAGTGAAGTGTCTCCAC 2700
QY 242 GluArgSerIleHisLeuPheIleAspSerLeuAsnGluGluAsnProSerIleAala 261
Db 2701 GAGCGCTCCATTCATCTCTTCATCGATCTCTGTTGATGAAGAAATCCAAAGTAAGGCC 2760
QY 262 TyrArgCysSerSerLysGluAlaPheGluLysGlyLeuCysLeuSerCysArgIleAsn 281
Db 2761 TACAGGTGCACTTCCAGGAAGCCTTTGAGAAAGGCTCTCTGTTGAGTTGAGAAAGAAC 2820
QY 282 ArgCysAsnAsnLeuGlyTyrGluIleAsnLysValArgAlaLysArgSerSerLysMet 301

Db 2821 CGCTGCAACAATCTGGGCTATGAGATCAATATAAGTCCAGCCAAAGACGACAAATG 2880
QY 302 TyrIleuYThrArgSerGlnMetProTyrLys 312
Db 2881 TACCTGAAGACTCGTTCTCAGATGCCCTACAAA 2913
RESULT 8
US-09-411-132A-2
; Sequence 2, Application US/09411132A
; Patent No. 6558936
; GENERAL INFORMATION:
; APPLICANT: Khodadoust, Mehran
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: No. 6558936el Human Lipase Proteins, Nucleic Acids Encoding
; TITLE OF INVENTION: Then, and Uses of Both of These
; FILE REFERENCE: 10147-14
; CURRENT APPLICATION NUMBER: US/09/411,132A
; CURRENT FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1401
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-411-132A-2
Alignment Scores: 1.84e-45 Length: 1401
Pred. No.: 461.50 Matches: 129
Score: 46.57% Conservative: 68
Percent Similarity: 46.57% Mismatches: 173
Best Local Similarity: 30.50% Indels: 53
Query Match: 19.35% Gaps: 14
DB: 4
US-10-019-341-3 (1-448) x US-09-411-132A-2 (1-1401)
QY 5 ArgAspPheIleAspIleGluSerLysPheAlaLeuArgThrProGluAspThrAlaGlu 24
Db 105 CAGGACTTCTCAACAGAGTGTGGTAGTTTACCTGCTCCAGAGAGAGATAAA----- 158
QY 25 AspThrCysHisLeuLeuProGlyValAlaGluSerValAlaThrCys----- 40
Db 159 -----CACTCGTTTCTCTCTACACTATACAAATCCCAATGCCCTATCAGGAGAT 209
QY 41 -----HisPheAsnHisSerSer-LysThrPhe----- 49
Db 210 CAGTGGGTAAATCTTCAACTATCCAGCCTCATATTTTGGAAACAGACAGATCACCCG 269
QY 50 -MetValIleHisGlyTyrThrValThrGlyMetTyrGluSerTyrValProLysLeuVa 69
Db 270 TATCAACATAGCTGGATGGAAACACAGATGGC-----AAATGGCAGAGACATGTG 320
QY 69 lAlaAlaLeuTyrLysArgGluProAspSerAsnValIleValValAspThrLeuSerAr 89
Db 321 CAATGTGTGTCTACAGCTGGAA---GATATAAATTCATTAAATTTAGATTGGATCAACGG 377
QY 89 gAlaGlnGluHisTyrProValSerAlaGlyTyrThrLysLeuValGlyGlnAspValAl 109
Db 378 TTCACGGGAA---TACATCATCTGTAAACAATCTCCGTGTGTGTGTGTGTGTGTGTGTGT 434
QY 109 aArgPheIleAsnTrpMetGluGluGluPheAsnTyrProLeuAspAsnValHisLeuLe 129
Db 435 TTATTTTATGATGTTCTCTCAATGAAATAATTTGAATATTTCCCTCTCTAAAGTGCATTTGAT 494
QY 129 uGlyTyrSerIleuGlyAlaHisAlaAlaGlyIleAlaGlySerLeuThrAsnLysVa 149
Db 495 TGGCCACAGCTTGGGAGCACACTGCTGGGAGAGCTGGGTTCAGGATA---CCAGGCCT 551
QY 149 lAsnArgIleThrGlyLeuAspProAlaGlyProAsnPheGluTyrAlaGluAlaProSe 169
Db 552 TGGAAAGTAATACTGGGTGGACCCAGCTGGGCCATTTTTCACAACTCCCAAGGAAGT 611

QY	169	rArgLeuSerProAspAlaAspValAspValLeuHisThr-----	184
Db	612	CAGGCTAGACCCCTCGATGCCAACTTTGTGACGTTATTCATACAAATGCAGCTCGCAT	671
QY	185	----PheThrArgGlySerProGlyArgSerIleGlnLysProValGlyHisVa	203
Db	672	CCTCTTTGAGCTTGGT-----GTTGAACCATTTGATGCTTGTGGTCACT	716
QY	203	lAspIleTyrProAsnGlyGlyThrPheGlnProGlyCysAsn-----IleGlyGluAl	221
Db	717	TGACITTTTACCAATATGNGGGAAGCACATGCCAGATGTGAAGACTTAATATACACCTTT	776
QY	221	alleArgValIleAlaGluArgGlyLeuGlyAspValAspGlnLeuValLysCysSerHi	241
Db	777	ACTGAAATTTAACTTCAATGCTTTACAAAAAGAAATGGCTTCCTTCTTTGACTGTACCA	836
QY	241	sGluArgSerIleHisLeuPheIleAspSerLeuLeuAsnGluGluAsnProSerLysAl	261
Db	837	TGCCGAAGTTATCAATTTTATGTGAAAGCAATCTTAATCTGTAT--GCATTTATTATGC	893
QY	261	aTyArgCysSerSerLysGluAlaPheGluLysGlyLeuCysLeuSerCysArgLysAs	281
Db	894	TTATCTTGATGATCCTACACATCTTTTAAAGCAGGAAATGCTTCTTTTGTCCAAAGA	953
QY	281	nArgCysAsnAsnLeuGlyTyrGluIleAsnLysValArgAlaLys-----Ar	297
Db	954	AGGTTGCCCAACAATGGTGCATTTTGCTGATAGATTTTCACITCAAATAATGAAGACTAA	1013
QY	297	gSerSerLysMetTyrLeuLysThrArgSerGlnMecProTyrLysValPheHisTyrGl	317
Db	1014	TGGATCACATTATTTTAAACACAGGGTCCCTTTCCCAATTCGCCGTTCGGAGCCAA	1073
QY	317	nValLysIleHisPheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGluIl	337
Db	1074	ATTGCTGTTAAACTCAGTGAAGCGAAGTC-----ACTCAAGGAACCTGTCTTTCT	1124
QY	337	eSerLeuTyrGlyThrValAlaGluSerGluAsnIleProPheThrLeuProGluValSe	357
Db	1125	TCGTGTAGCGGGCAATTGGAAAACTGGGAGCTTTGCCATTGCTAGTGGAAAACTTGA	1184
QY	357	rThrAsnLysThrTyrSerPheLeuIleTyrThrGluValAspIleGlyLeuLeuMe	377
Db	1185	GCCAGGCATGACTTACACAAAAATAATCGATCGACAGGTTAAACGTTCGAAACATTACA	1244
QY	377	LeuLysLeuLysTrpLys-----SerAspSerTyr-PheSerTyrSerAspt	393
Db	1245	TGTTCACTTCATCTGGAAAAACAATTGTTTGAAGATTCTCAGAATAAGTTGGAGCAGA	1304
QY	393	rpTrp	394
Db	1305	AATGG	1309

RESULT. T 9

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RESOL1 9
US-09-411-132A-1
; Sequence 1, Application US/09411132A
; Patent No. 6558936
; GENERAL INFORMATION:
; APPLICANT: Khodadoust, Mehran
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: No. 6558936el Human Lipase Proteins, Nucleic Acides Encoding
; TITLE OF INVENTION: Them, and Uses of Both of These
; FILE REFERENCE: 10147-14
; CURRENT APPLICATION NUMBER: US/09/411.132A
; CURRENT FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2352
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (2159)

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[illegible]

Mon Oct 25 15:42:53 2004

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; NAME/KEY: UNSURE
; LOCATION: 305
; OTHER INFORMATION: Xaa=Pro or Thr
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 376
; OTHER INFORMATION: Xaa= * or Gly
US-09-513-999C-79
Alignment Scores:
Pred. No.: 2,3e-44 Length: 1206
Score: 451.50 Matches: 108
Percent Similarity: 49.71% Conservative: 64
Best Local Similarity: 31.21% Mismatches: 155
Query Match: 18.93% Indels: 19
DB: 4 Gaps: 9
US-10-019-341-3 (1-448) x US-09-513-999C-79 (1-1206)
Qy 9 AspIleGluSerLysPheAlaLeuArgThrProGluAspThrAlaGluAspThrCysHis 28
Db 177 GATGTCACACCCCGCTTCTCTATATATAATGAGAAC-----CCAAACAACATTTCAA 230
Qy 29 LeuIleProGlyValAlaGluSerValAlaThrCysHisPheAsnHisSerSerLysThr 48
Db 231 GAAGTTGCCGCGAGATTTCATCAAGCATCAGTGGCTCCCAATTTCAAACAATAAGAAAACT 290
Qy 49 PheMetValIleHisGlyTrpThrValThrGlyMetTyrGluSerTrpValProLysLeu 68
Db 291 CGCTTTATTATTTCGA-----TTCATAGACAGGAGGAGAGAAACTGGCTGCCCAATGG 344
Qy 69 ValAlaAlaLeuTyrLysArgGluProAspSerAsnValIleValValAspTrpLeuSer 88
Db 345 TCAAGAGATCTGTTTCAGGTGGAA---AGTGGAACCTGTATCTGTGTGACTGGAAAGGT 401
Qy 89 ArgAlaGlnGluHisTyrProValSerAlaGlyTyrThrLysLeuValGlyGlnAspVal 108
Db 402 GGCTCCGAACTGGATACACACAAGCTCGCAGAACATCAGGATCGTGGAGCAGAAAGTG 451
Qy 109 AlaArgPheIleAsnTrpMetGluGluGluPheAsnTyrProLeuAspAsnValHisLeu 128
Db 462 GCATATTTTGTGAAATTTCTTCAGTCGGCGTTTGGTTACTCACCITCCCAATGGCATGTC 521
Qy 129 LeuGlyTyrSerLeuGlyAlaHisAlaAlaGlyIleAlaGlySerLeuThrAsnLysLys 148
Db 522 ATTGGCCACAGCTGGTGGTCCACACGCTGCTGGGGAGGCTGGAAGAGAGAACCAATGGGACC 581
Qy 149 ValAsnArgIleThrGlyLeuAspProAlaGlyProAsnPheGluTyrAlaGluAlaPro 168
Db 582 ATTGGACGCATCACAGGGTTGGACCCAGCAGAACCTTGCTTTTCAGGGCACACCTGAATTA 641
Qy 169 SerArgLeuSerProAspAspAlaAspPheValAspValLeuHisThrPheThrArgGly 188
Db 642 GTCCGATTGGACCCCGGATGCGAAATTTGTGGATGTAATTCAC-----ACGGATGGT 695
Qy 189 Ser-----ProGlyArgSerIleGlyIleGlnLysProValGlyHisValAspIle 205
Db 696 GCGCCCATAGTCCCAATTTGGGGTTTGGAAATGAGCAAGCTGGTGGCCCACTAGATTC 755
Qy 206 TyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGluAlaIleArgValIle 225
Db 756 TTTCCTCAATGGAGGAGTGGAAATGCCCTGGAGTGTAAAAAGAACACATCTCTCTCAGATTGTG 815
Qy 226 AlaGluArgGlyLeuGlyAsp---ValAspGlnLeuValLysCysSerHisGluArgSer 244
Db 816 GACATAGACGAATCTGGGAGGAGGACTCGAGACTTTTGGCGCTGTATATCACTTAAGAAGC 875
Qy 245 IleHisLeuPheIleAspSerLeuLeuAsnGluGluAsnProSerLysAlaTyrArgCys 264
Db 876 TACAAATATTACACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 932
Qy 265 SerSerLysGluAlaPheGlyLysGlyLeuSerCysArgLysAsnArgCysAsn 284

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; NAME/KEY: UNSURE
; LOCATION: 305
; OTHER INFORMATION: Xaa=Pro or Thr
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 376
; OTHER INFORMATION: Xaa= * or Gly
US-09-513-999C-79
Alignment Scores:
Pred. No.: 2,3e-44 Length: 1206
Score: 451.50 Matches: 108
Percent Similarity: 49.71% Conservative: 64
Best Local Similarity: 31.21% Mismatches: 155
Query Match: 18.93% Indels: 19
DB: 4 Gaps: 9
US-10-019-341-3 (1-448) x US-09-513-999C-79 (1-1206)
Qy 9 AspIleGluSerLysPheAlaLeuArgThrProGluAspThrAlaGluAspThrCysHis 28
Db 177 GATGTCACACCCCGCTTCTCTATATATAATGAGAAC-----CCAAACAACATTTCAA 230
Qy 29 LeuIleProGlyValAlaGluSerValAlaThrCysHisPheAsnHisSerSerLysThr 48
Db 231 GAAGTTGCCGCGAGATTTCATCAAGCATCAGTGGCTCCCAATTTCAAACAATAAGAAAACT 290
Qy 49 PheMetValIleHisGlyTrpThrValThrGlyMetTyrGluSerTrpValProLysLeu 68
Db 291 CGCTTTATTATTTCGA-----TTCATAGACAGGAGGAGAGAAACTGGCTGCCCAATGG 344
Qy 69 ValAlaAlaLeuTyrLysArgGluProAspSerAsnValIleValValAspTrpLeuSer 88
Db 345 TCAAGAGATCTGTTTCAGGTGGAA---AGTGGAACCTGTATCTGTGTGACTGGAAAGGT 401
Qy 89 ArgAlaGlnGluHisTyrProValSerAlaGlyTyrThrLysLeuValGlyGlnAspVal 108
Db 402 GGCTCCGAACTGGATACACACAAGCTCGCAGAACATCAGGATCGTGGAGCAGAAAGTG 451
Qy 109 AlaArgPheIleAsnTrpMetGluGluGluPheAsnTyrProLeuAspAsnValHisLeu 128
Db 462 GCATATTTTGTGAAATTTCTTCAGTCGGCGTTTGGTTACTCACCITCCCAATGGCATGTC 521
Qy 129 LeuGlyTyrSerLeuGlyAlaHisAlaAlaGlyIleAlaGlySerLeuThrAsnLysLys 148
Db 522 ATTGGCCACAGCTGGTGGTCCACACGCTGCTGGGGAGGCTGGAAGAGAGAACCAATGGGACC 581
Qy 149 ValAsnArgIleThrGlyLeuAspProAlaGlyProAsnPheGluTyrAlaGluAlaPro 168
Db 582 ATTGGACGCATCACAGGGTTGGACCCAGCAGAACCTTGCTTTTCAGGGCACACCTGAATTA 641
Qy 169 SerArgLeuSerProAspAspAlaAspPheValAspValLeuHisThrPheThrArgGly 188
Db 642 GTCCGATTGGACCCCGGATGCGAAATTTGTGGATGTAATTCAC-----ACGGATGGT 695
Qy 189 Ser-----ProGlyArgSerIleGlyIleGlnLysProValGlyHisValAspIle 205
Db 696 GCGCCCATAGTCCCAATTTGGGGTTTGGAAATGAGCAAGCTGGTGGCCCACTAGATTC 755
Qy 206 TyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGluAlaIleArgValIle 225
Db 756 TTTCCTCAATGGAGGAGTGGAAATGCCCTGGAGTGTAAAAAGAACACATCTCTCTCAGATTGTG 815
Qy 226 AlaGluArgGlyLeuGlyAsp---ValAspGlnLeuValLysCysSerHisGluArgSer 244
Db 816 GACATAGACGAATCTGGGAGGAGGACTCGAGACTTTTGGCGCTGTATATCACTTAAGAAGC 875
Qy 245 IleHisLeuPheIleAspSerLeuLeuAsnGluGluAsnProSerLysAlaTyrArgCys 264
Db 876 TACAAATATTACACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 932
Qy 265 SerSerLysGluAlaPheGlyLysGlyLeuSerCysArgLysAsnArgCysAsn 284

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Db 933 GCCTCTTACAACTCTTCACTGCAACAACTGTTTCCCTTGTCCAAGTGGAGGTCGCMCA 992
 QY 285 AsnLeuGlyTyrGluIleAsnLysValArgAlaIysArgSer-----SerLysMet 301
 Db 993 CAGATGGGTCACCTATCTGTATAGATATCTCGGGAACAATAATGATGGGCCAGAAATTT 1052
 QY 302 TyrLeuLysThrArgSerGlnMetProTyrLysValPheHisTyrGlnValLysIleHis 321
 Db 1053 TATCTAGACACTGTGTATGTCAGTAATTTTGCACGTTGGAGGTATAAGGTATCTGTACA 1112
 QY 322 PheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGluLysSerLeuTyrGly 341
 Db 1113 CTGCTCTGGAATAAGGTTACAGACAC-----ATACTAGTTCTTTGTTCCGA 1160
 QY 342 ThrValAlaGluSerGlu 347
 Db 1161 AATAAGGAACCTCTAAG 1178

RESULT 11

US-08-905-124-4
 ; Sequence 4, Application US/08905124
 ; Patent No. 6074825
 ; GENERAL INFORMATION:
 ; APPLICANT: Rundell, Clark A.
 ; APPLICANT: Vary, Calvin P.H.
 ; TITLE OF INVENTION: STABLE ENCAPSULATED REFERENCE
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Wood, Herron & Evans, L.L.P.
 ; STREET: 2700 Carew Tower
 ; CITY: Cincinnati
 ; STATE: OH
 ; COUNTRY: USA
 ; ZIP: 45202-2917
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows DEMONSTRATION Version 2.0D
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/905,124
 ; FILING DATE: 31-JUL-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Frei, Donald F
 ; REGISTRATION NUMBER: 21,190
 ; REFERENCE/DOCKET NUMBER: CASI-02
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 513-241-2324
 ; TELEFAX: 513-421-7269
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 231 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: Genomic DNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: human
 ; CELL TYPE: lymphocyte
 US-08-905-124-4
 Alignment Scores:
 Pred. No.: 4,63e-41 Length: 231
 Score: 414.00 Matches: 77
 Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 17.36% Indels: 0
 DB: 3 Gaps: 0
 US-10-019-341-3 (1-448) x US-08-905-124-4 (1-231)
 QY 154 GlyLeuAspProAlaGlyProAsnPheGluTyrAlaGluAlaProSerArgLeuSerPro 173
 Db 1 GGCTCTGATCCAGCTCGACCTAACTTTTGAATATGCAGAGGCCCGAGTCTGCTTTCTCCT 60
 QY 174 AspAspAlaAspPheValaspValLeuHisThrArgGlySerProGlyArgSer 193
 Db 61 GATGATGCGAGATTTTGTAGACCTTTACACACATTCCACAGAGGTCCTCGTGTGGAAGC 120
 QY 194 IleGlyIleGlnLysProValGlyHisValAspIleTyrProAsnGlyGlyThrPheGln 213
 Db 121 ATTGAATCCAGAACCACTGTGGGATGTTGACATTTACCCGAATGGAGGACTT 231
 QY 214 ProGlyCysAsnIleGlyGluAlaIleArgValIleAlaGluArgGlyLeu 230
 Db 181 CCAGGATGTAACTTGGAGAGCTATCCGCGTGATTGCAGAGAGGACTT 231

RESULT 12

US-09-799-451-90
 ; Sequence 90, Application US/09799451
 ; Patent No. 6783969
 ; GENERAL INFORMATION:
 ; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Zhou, Ping
 ; APPLICANT: Goodrich, Ryle
 ; APPLICANT: Asundi, Vinod
 ; APPLICANT: Ren, Feiyun
 ; APPLICANT: Zhang, Jie
 ; APPLICANT: Xue, Aidong J.
 ; APPLICANT: Zhao, Qing A.
 ; APPLICANT: Wang, Jian-Rui
 ; APPLICANT: Ma, Yungqing
 ; APPLICANT: Yamazaki, Victoria
 ; APPLICANT: Chen, Rui-hong
 ; APPLICANT: Wang, Zhiwei
 ; APPLICANT: Wang, Dunrui
 ; APPLICANT: Yang, Yonghong
 ; APPLICANT: Wehrman, Tom
 ; APPLICANT: Ghosh, Reena
 ; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
 ; TITLE OF INVENTION: Polypeptides
 ; FILE REFERENCE: 803
 ; CURRENT APPLICATION NUMBER: US/09/799,451
 ; CURRENT FILING DATE: 2001-03-05
 ; NUMBER OF SEQ ID NOS: 948
 ; SOFTWARE: pt_FL_genes Version 2.0
 ; SEQ ID NO 90
 ; LENGTH: 1889
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (366)..(1334)
 US-09-799-451-90
 Alignment Scores:
 Pred. No.: 2,54e-33 Length: 1889
 Score: 363.00 Matches: 101
 Percent Similarity: 42.98% Conservative: 46
 Best Local Similarity: 29.53% Mismatches: 89
 Query Match: 15.22% Indels: 106
 DB: 4 Gaps: 13
 US-10-019-341-3 (1-448) x US-09-799-451-90 (1-1889)
 QY 111 PheIleAsnTrpMetGluGluPheAsnTyrProLeuAspAsnValHisLeuLeuGly 130

Mon Oct 25 15:42:53 2004

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; Patent No. 5593877
; GENERAL INFORMATION:
; APPLICANT: King, Te-Piao
; TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF
; TITLE OF INVENTION: VESPID VENOM ENZYMES, SUCH AS PHOSPHOLIPASE AND
; TITLE OF INVENTION: HYALURONIDASE, AND IMMUNOLOGICAL THERAPIES BASED
; TITLE OF INVENTION: THEREON
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESS: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/180,209B
; FILING DATE: 11-JAN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/031,400
; FILING DATE: 11-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-074 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1050 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..951
; US-08-180-209B-16

Alignment Scores:
Pred. No.: 1,38e-29 Length: 1050
Score: 328.50 Matches: 87
Percent Similarity: 43.49% Conservative: 50
Best Local Similarity: 27.62% Mismatches: 96
Query Match: 13.77% Indels: 82
DB: 1 Gaps: 10

US-10-019-341-3 (1-448) x US-08-180-209B-16 (1-1050)

QY 43 AsnHisSerSerLysThr-PheMetValIleHisGlyTyrThrValThrGlyMetTyrG1 62
Db 171 AATCATAAACAGCTCCAGTGTGTTATTCATACGATGGTTTACITCGTCTGCAACCGAAA 230
QY 62 uSerTrpValProLysLeuValAlaLeuTyrLysArgGluProAspSerAsnVal11 82
Db 231 AAATTCGTTCATGTATGTCAGAGGCTCTATGTCAT-----ACAGGTGATTTCTTATAAT 284
QY 82 eValValAspTrp---LeuSerArgAlaGlnGluHisTyrPro----- 95
Db 285 TATGTCGATTTGGCGGATGGCTGTCTGTACTGTAATAACCGAGTCTGAGTATATGTT 344
QY 96 -----ValSerAlaGlyTyrThrLysLeuValGlyGlnAspValAlaArgPheIleAs 113
Db 345 TTATAAGGCTCCCGTTGGTAATACACGCTTAGTTGGAATTTTATCGTATGATCGCAAA 404

; RESULT 13
; US-08-180-209B-16
; Sequence 16, Application US/08180209B

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QY 113 nTrpMetGluGluPheAsnTyrProLeuAspAsnValHisLeuLeuGlyTyrSerLe 133
Db 405 GAAACTTGTAGAACAAATATAAGTCCGATGACAAATATACGATCTGGTGGACACAGTTT 464
QY 133 uGlyAlaHisAlaAlaGlyLeuAlaGlySerLeuThrAsnLys-----LysVa 149
Db 465 GGGCGCACACATTTTCAGGTTTCGAGGACAAAGAGTTCAAGAGTTAAATTTAGGAAATTT 524
QY 149 lAsnArgIleThrGlyLeuAspProAlaGlyProAsnPheGluTyrAlaGluAlaProSe 169
Db 525 TTCTGAAATATTGGGCTTGATCTGCTGGCCCTAGTTTCAAGAAATGATTTGTTCCGA 584
QY 169 rArgLeuSerProAspAspAlaAspPheValAspValLeuHisThrPheThrArgGlySe 189
Db 585 GAGAAATCTGGAGACAGACGACATATATGACAAATTTTACATACA-----630
QY 189 rProGlyArgSerIleGlyLeuGlnLysProValGlyHisValAspIleTyrProAsnGl 209
Db 631 ----TCGACGATTTAGGAACAGAGAACTCTTGGCACCGCTGATTTCTACATAATAA 686
QY 209 yGlyThrPheGlnProGlyCysAsn-----lIleGlyGluAlaAlaArgValIleAlaGl 227
Db 687 CGGAAGTAATCAACCGGTTGCAGATATATTATGGAGAACT-----729
QY 227 uArgGlyLeuGlyAspValAspGlnLeuValLysCysSerHisGluArgSerIleHisLe 247
Db 730 ----TGCTCTCATACGAGACCGGTGAATA 755
QY 247 uPheIleAspSerLeuLeuAsnGlu-----GluAsnPr 258
Db 756 CTTTACCGAGTGCATAAGACGGCATGTGTTTAATTGGGTCGCCGAGTCCCAAGAAATCC 815
QY 258 oSerLysAlaTyrArgCysSerSerLysGluAlaPheGluLysGlyLeuCysLeuSerCy 278
Db 816 GCAGCTGTGTTGGAAGTCACAGAACGAGTGGCTTTGCGTTGGATTAAACGCAAGAA 875
QY 278 sArgLysAsnArg-----CysAsnAs 285
Db 876 ATATCCTAAAGGGGCTCATTTTATGATACCGGTTGAAGCTGAAGCTCCATATTCGAATA 935
QY 285 mLeuGlyTyr-----288
Db 936 CAACGGGAATAATTAATTATATAAAAAACATTAATTGACACAAGTGCAATTTGT 995
QY 289 ----GluIleAsnLysValArgAlaLysArgSerSerLys 300
Db 996 TAATGATGAATGAATAATACGATTCAAGAAAGAAAAA 1038

RESULT 14
US-08-385-745-16
; Sequence 16, Application US/08385745
; Patent No. 5612209
; GENERAL INFORMATION:
; APPLICANT: King, Te Piao
; TITLE OF INVENTION: Cloning and Recombinant Production of
; TITLE OF INVENTION: Vespid Venom Phospholipases, and Immunological Therapies
; TITLE OF INVENTION: Based Thereon
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/385,745
; FILING DATE:
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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/031,400
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 3288-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1050 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..951
; US-08-385-745-16

Alignment Scores:
Pred. No.: 1.38e-29 Length: 1050
Score: 328.50 Matches: 87
Percent Similarity: 43.49% Conservativeness: 50
Best Local Similarity: 27.62% Mismatches: 96
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US-10-019-341-3 (1-448) x US-08-385-745-16 (1-1050)
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QY 62 uSerTrpValProLysLeuValAlaLeuTyrLysArgGluProAspSerAsnValIl 82
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QY 82 eValValAspTrp---LeuSerArgAlaGlnGluHisTyrPro-----95
Db 285 TATGTCGATTTGGCGGATGGCTGCTGTACTGTAATACCGAGTCTGAGCTATATGTT 344
QY 96 -----ValSerAlaGlyTyrThrLysLeuValGlyGlnAspValAlaArgPheIleAs 113
Db 345 TTATAAGGCTCCCGTTGGTAATACACGCTTAGTTGGAAATTTTATCGCTATGTCGAAA 404
QY 113 nTrpMetGluGluPheAsnTyrProLeuAspAsnValHisLeuLeuGlyTyrSerLe 133
Db 405 GAAACTTGTAGAACAAATATAAGTCCGATGACAAATATACGATCTGGTGGACACAGTTT 464
QY 133 uGlyAlaHisAlaAlaGlyLeuAlaGlySerLeuThrAsnLys-----LysVa 149
Db 465 GGGCGCACACATTTTCAGGTTTCGAGGACAAAGAGTTCAAGAGTTAAATTTAGGAAATTT 524
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Db 585 GAGAAATCTGGAGACAGACGACATATGACAAATTTTACATACA-----630
QY 189 rProGlyArgSerIleGlyLeuGlnLysProValGlyHisValAspIleTyrProAsnGl 209
Db 631 ----TCGACGAAATTTAGGAACAGAGAACTCTTGGCACCGCTGATTTCTACATAATAA 686
QY 209 yGlyThrPheGlnProGlyCysAsn-----lIleGlyGluAlaAlaArgValIleAlaGl 227
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Mon Oct 25 15:42:53 2004

us-10-019-341-3.rni

MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..951
US-08-485-388-16

Alignment Scores:
Pred. No.: 1,388-29 Length: 1050
Score: 328.50 Matches: 87
Percent Similarity: 43.49% Conservative: 50
Best Local Similarity: 27.62% Mismatches: 96
Query Match: 13.77% Indels: 82
DB: 3 Gaps: 10

US-10-019-341-3 (1-448) x US-08-485-388-16 (1-1050)

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DB 171 AATCATAAAGCTCCAGTTGTATTACATACGATGGTTTACTTCTGTCGACCGAATA 230
QY 62 userTrpValProLysLeuValAlaLeuTyrLysArgGluProAspSerAsnValIle 82
DB 231 AAATTTCTGTTGCTATGTCTAGAGGCTCTTATGCAAT-----ACAGGTGATTTTCTTATAAT 284
QY 82 eValValAspTrp---LeuSerArgAlaGlnGluHisTyrPro----- 95
DB 285 TATGTTGATTTGGCGGATGGCTGTGTACTGATGAATACCCAGGTCTGAAGTATATGTT 344
QY 96 -----ValSerAlaGlyTyrThrLysLeuValGlyGlnAspValAlaAargPheIleAs 113
DB 345 TTATAAGGCTGCCGTTGTGTAATACACGCTTAGTTGGAATTTTATCGCTATGATCGCAAA 404
QY 113 nTrpMetGluGluGluPheAsnTyrProLeuAspAsnValHisLeuLeuGlyTyrSerLe 133
DB 405 GAACTTTAGAACATAATATAAGTCCGATGACAAATATACGACTCGTGGGACACAGTTT 464
QY 133 uGlyAlaHisAlaAlaGlyIleAlaGlySerLeuThrAsnLys-----LysVa 149
DB 465 GGGCGCACACATTTTCAGGTTTCGACGCAAAAGAGTTCAAGAGTTAAATAGGAATTT 524
QY 149 lAsnArgIleThrGlyLeuAspProAlaGlyProAsnPheGluTyrAlaGluAlaProSe 169
DB 525 TTCTGAAATTTATTTGGGCTTGTATCTCTGCTGGGCTAGTTTCAAGAAAATGATTTGCCGA 584
QY 169 rArgLeuSerProAspAspAlaAspPheValAspValLeuHisThrPheThrArgGlySe 189
DB 585 GAGAACTCGGAGACAGACACCATATATGTACAAATTTTACATACA----- 630
QY 189 rProGlyArgSerIleGlyIleGlnLysProValGlyHisValAspIleTyrProAsnGl 209
DB 631 ----TCGAGCAATTTAGAACACAGAGAGAACTCTTGGCAGCGTCTGATTTCTACATAATAA 686
QY 209 yGlyThrPheGlnProGlyCysAsn-----IleGlyGluAlaIleArgValIleAlaGl 227
DB 687 CGGAAGTAATCAACCCGGTTGCAATATATTTGGAGAACT----- 729
QY 227 uArgGlyLeuGlyAspValAspGlnLeuValLysCysSerHisGluArgSerIleHisLe 247
DB 730 -----TGCTCTCATACGAGAGCGGTGAATA 755
QY 247 uPheIleAspSerLeuLeuAsnGlu-----GluAsnPr 258
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QY 258 oSerLysAlaTyrArgCysSerSerLysGluAlaPheGluLysGlyLeuCysLeuSerCy 278
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QY 278 sArgLysAsnArg-----CysAsnAs 285
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RESULT 15

US-08-485-388-16
Sequence 16, Application US/08485388
Patent No. 6270763
GENERAL INFORMATION:
APPLICANT: King, Te Piao
TITLE OF INVENTION: Cloning and Recombinant Production of
TITLE OF INVENTION: Vespid Venom Phospholipases, and Immunological Therapies
TITLE OF INVENTION: Based Thereon
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,388
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/385,745
FILING DATE: 08-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/031,400
FILING DATE: 11-MAR-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-074 FWCA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1050 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

QY 227 uArgGlyLeuGlyAspValAspGlnLeuValLysCysSerHisGluArgSerIleHisLe 247
DB 730 -----TGCTCTCATACGAGAGCGGTGAATA 755
QY 247 uPheIleAspSerLeuLeuAsnGlu-----GluAsnPr 258
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QY 258 oSerLysAlaTyrArgCysSerSerLysGluAlaPheGluLysGlyLeuCysLeuSerCy 278
DB 816 GCAGCCTGTTTCGAAGTGCACAGAAACGAGTGGCGTTTGGCTGGATTAAACGCAAGAA 875
QY 278 sArgLysAsnArg-----CysAsnAs 285
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Db      936  CAACGGGAAATAATTTAATTATATAAAAAAACATTACTATTGACACAAGTGCAATTGT 995
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 Job time : 143 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: October 24, 2004, 18:24:55 ; Search time 678 Seconds
(without alignments)

3385.718 Million cell updates/sec

Title: US-10-019-341-3

Perfect score: 2385

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Searched: 3407233 seqs, 2561960514 residues

Total number of hits satisfying chosen parameters: 6814466

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	2385	100.0	3549	17	US-10-755-889-99
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6	2372	99.5	4075	10	US-09-971-392-107
7	2235.5	93.7	3617	16	US-10-388-934-188
8	1161	48.7	2565	15	US-10-128-449A-7
9	1161	48.7	3927	15	US-10-354-358-45
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ALIGNMENTS

RESULT 1

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; Sequence 2217, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Can
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR FILING DATE: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26

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7  P R I O R   F I L I N G   D A T E :   2 0 0 0 - 0 9 - 2 7
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11 P R I O R   F I L I N G   D A T E :   2 0 0 0 - 0 9 - 2 7
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13 P R I O R   A P P L I C A T I O N   N U M B E R :   U S / 6 0 / 2 3 5 , 8 4 0
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15 P R I O R   F I L I N G   D A T E :   2 0 0 0 - 0 9 - 2 7
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17 P R I O R   A P P L I C A T I O N   N U M B E R :   U S / 6 0 / 2 3 5 , 8 6 3
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21 N U M B E R   O F   S E Q   I D   N O S :   2 2 7 6
22
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24
25 S E Q   I D   N O   2 2 1 7
26
27 L E N G T H :   3 5 4 9
28
29 T Y P E :   D N A
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33 U S - 0 9 - 9 5 4 - 4 5 6 - 2 2 1 7

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Best Overall Similarity:	100.00%	
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	Mismatches:	0
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DB	376	CATTTCATTCACAGCAGCAAAACCTTTCATGTGTGATCCTCATGCTGCAGCGTTAACGAATG	435
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QY	101	ThrIysLeuValGlyGlnAspValAlaArgPheIleAsnTyrMetGluGluGluPheAsn	120
DB	556	ACCAAACCTGGTGGGACAGGATGTGGCCCGGTTTATCAACTGGATCGAGGAGAGATTAAAC	615
QY	121	TyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeuGlyValAlaHisAlaAlaGlyIle	140
DB	616	TACCCCTCTGGACAAATGTCCATCTCTGGGATACAGCCTTGGAGCCCATGCTGTGCGATT	675
QY	141	AlaGlySerLeuThrAsnIlySylsValAsnArgIleThrGlyLeuAspProAlaGlyPro	160
DB	676	GCAGGAAGTCTCACCAATAAGAAAGTCAACAGAAATTTACTGGCTCGATCCAGCTGGACCT	735
QY	161	AsnPheGluTyrAlaGluAlaProSerArgLeuSerProAspAlaAspPheValAsp	180
DB	736	AACTTTGATGTGCAGAACCCCGAGTGTCTTCTCTGATGATGCAGATTTGTAGAC	795
QY	181	ValLeuHisThrPheThrArgGlySerProGlyArgSerIleGlyIleGlnIysProVal	200
DB	796	GTCTTTACACACTTCACAGAGGGTCCCTGTGTCGAAGCAVTTGGAAATCCAGAAACCAAGTT	855
QY	201	GlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGlu	220
DB	856	GGGCATGTTGACATTTTACCCGAATGGAGGTACTTTTACGCCAGGATGTAACTTGGAGAA	915
QY	221	AlaIleArgValIleAlaGluArgGlyLeuGlyAspValAspGlnLeuValIysCysSer	240

916	GCTATCCGGGTGATTCCAGAGAGGACTTGGAGATGTGGACCAGCTAGTGAAGTGTCTCC	975
241	HisGluArgSerIleHisLeuPheIleAspSerLeuLeuAsnGluGluAsnProSerIys	260
976	CACAGGGCTCCATTTCATCTCTCATCGACTCTCTGTTGAATGAAGAAATCCAAGTAAG	1035
261	AlaTyrArgCysSerSerIysGluAlaPheGluLysGlyLeuCysLeuSerCysArgIys	280
1036	GCCTACAGGTGTCAGTGTCCCAAGGAAGCCTTTGGAAAGGGCTCTGCTTGAGTTGTGAAGAAG	1095
281	AsnArgCysAsnAsnLeuGlyTyrGluIleAsnLysValAlaLysArgSerSerIys	300
1096	AACCGCTGCACAACTCTGGCTATGAGATCAATAAGTCAGAGCCAAAAGAGCAGCAAA	1155
301	MetTyrLeuIysThrArgSerGlnMetProTyrLysValPheHisTyrGlnValIysIle	320
1156	ATGTACCTGAAGACTCGTCTCAGATGCCCTACAAAGTCTTCCATTACCAAGTAAAGATT	1215
321	HisPheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGluIleSerLeuTyr	340
1216	CAITTTTCTGGGACTGAGAGTGAACCCATACCATTACAGCCCTTTCAGATTCTCTGTAT	1275
341	GlyThrValAlaGluSerGluAsnIleProPheThrLeuProGluValSerThrAsnLys	360
1276	GGCACCCGTGGCCGAGAGTGAGAACATCCCATTCACCTCTGCCTGAAGTTTCCACAAATAAG	1335
361	ThrTyrSerPheLeuIleTyrThrGluValAspIleGlyCyluLeuLeuMetLeuLysLeu	380
1336	ACCTACTCCCTCTCTTAATTTACAGAGAGTATGATTTGGAGAACTACTCATGTTGAAGCTC	1395
381	LysTrpIysSerAspSerTyrPheSerTrpSerAspTrpTrpSerProGlyPheAla	400
1396	AAATGGAAAGAGTGATTCATCTTTAGCTGGTCAGACTGGTGGAGCAGCTCCGGCTTCGCC	1455
401	IleGlnIysIleArgValLysAlaGlyGluThrGlnIysIysValIlePheCysSerArg	420
1456	ATTCAGAAGATCAGAGTAAAGCAGGAGAGACTCAGAAAAAGGTGATCTTCTGTTCCTAGG	1515
421	GlnIysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHisAsp	440
1516	GAGAAAGTGTCTCATTTTCAGAAAGGAAAGGCACCTCGGGTATTTGTGAAATGCCATGAC	1575
441	LysSerLeuAsnLysLysSerGly	448
1576	AGTCTCTGAATAAGTCAAGTCAGGC	1599

RESULT 2

```

US-09-802-640-13
Sequence 13, Application US/09802640
Publication No. US20030036057A1
GENERAL INFORMATION:
APPLICANT: Braun, Andreas
APPLICANT: Bonsal Aruna
APPLICANT: Kleyn Patrick
TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND THEIR USE
FILE REFERENCE: 24736-2048
CURRENT APPLICATION NUMBER: US/09/802,640
CURRENT FILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 122
SOFTWARE: fastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 3549
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: CDS
LOCATION: (175)...(1602)
OTHER INFORMATION: Nucleotide sequence encoding lipoprotein lipase
OTHER INFORMATION: (LPL)
US-09-802-640-13

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US-09-802-640-13

Alignment Scores:

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Pred. No.: 5,18e-277 Length: 3549
Score: 2385.00 Matches: 448
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-019-341-3 (1-448) x US-09-802-640-13 (1-3549)

QY 1 AlaAspGlnArgAspPheIleAspIleGluSerLysPheAlaLeuArgThrProGlu 20
   |||||
Db 256 GCCGACCAAGAGAGATTTATCGACATCGAAGTAAATTTGCCCTAAGGACCCCTGAA 315

QY 21 AspThrAlaGluAspThrCysHisLeuIleProGlyValAlaGluSerValAlaThrCys 40
   |||||
Db 316 GACACAGCTGAGGACACTTGCACCTCATTTCCGGAGTAGCAGAGTCGCTGGCTACCTGT 375

QY 41 HisPheAsnHisSerLysThrPheMetValIleHisGlyTyrThrValThrGlyMet 60
   |||||
Db 376 CATTTCAATCACAGCAGCAAAACCTTCATGGTGATCCATGGCTGGAGCGGTACAGGAATG 435

QY 61 TyrGluSerTrpValProLysLeuValAlaAlaLeuTyrLysArgGluProAspSerAsn 80
   |||||
Db 436 TATGAGAGTTGGGTGCCAAACTTTGGCGGCCCTGTACAAGAGAGAACCCAGACTCCAAT 495

QY 81 ValIleValAlaAspTrpLeuSerArgAlaGlnGluHisTyrProValSerAlaGlyTyr 100
   |||||
Db 496 GTCAATGTGGTGACCTGGCTGTACGGGCTCAGGAGCATTACCCAGTGTCCGCGGCTAC 555

QY 101 ThrLysLeuValGlyGlnAspValAlaArgPheIleAsnTrpMetGluGluGluPheAsn 120
   |||||
Db 556 ACCAACTGGTGGGACAGATGTGCCCGTTTATCACTCGATGGAGGAGAGTTTAAAC 615

QY 121 TyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeuGlyAlaHisAlaGlyIle 140
   |||||
Db 616 TACCCTCTGGCAATGTCCATCTCTGGGATACAGCCTTGGAGCCATGCTGCTGGCAT 675

QY 141 AlaGlySerLeuThrAsnLysLysValAsnArgIleThrGlyLeuAspProAlaGlyPro 160
   |||||
Db 676 CGAGAACTCTGACCAATAGNAAGTCAACAGAAATTACTGGCTCGATCCAGCTGGAGCT 735

QY 161 AsnPheGluTyrAlaGluAlaProSerArgLeuSerProAspAspAlaAspPheValAsp 180
   |||||
Db 736 AACTTTGAGTATCGAAGACCCGAGTGTCTTCTCTGATGATGACAGATTTGTAGAC 795

QY 181 ValLeuHisThrPheThrArgGlySerProGlyArgSerIleGlyIleGlnLysProVal 200
   |||||
Db 796 GTCTTACACATTCACCAGAGGGTCCCTCGTGAAGCATTTGGAATCCAGAAACCAAGT 855

QY 201 GlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGlu 220
   |||||
Db 856 GGGCATGTTGACATTTACCCGAAATGGAGGTACTTTTCAGCCAGGATGTAAACATTTGGAGAA 915

QY 221 AlaIleArgValIleAlaGluArgGlyLeuGlyAspValAspGlnLeuValLysCysSer 240
   |||||
Db 916 GCTATCGCGGTGATTCAGACAGAGAGGACTTGGAGATGTGGACAGCTAGTGAAGTGTCTCC 975

QY 241 HisGluArgSerIleHisLeuPheIleAspSerLeuLeuAsnGluGluAsnProSerLys 260
   |||||
Db 976 CACGAGCGCTCAATTCATCTCTTCATGACTCTCTGTTGAATGAAGAAATCCCAAGTAAG 1035

QY 261 AlaTyrArgCysSerSerLysGluAlaPheGluLysGlyLeuCysLeuSerCysArgLys 280
   |||||
Db 1036 GCCTACAGGTGCAGTTCCAAGGAAGCCCTTTGAGAAAGGGCTCTGCTTGTAGTGTAGAAAG 1095

QY 281 AsnArgCysAsnAsnLeuGlyTyrGluIleAsnLysValArgAlaLysArgSerSerLys 300
   |||||
Db 1096 AACCGCTGCCAAATCTGGGCTATGAGATCAATAAAGTCAGAGCCAAAGAGACGAGAA 1155

QY 301 MetTyrLeuLysThrArgSerGlnMetProTyrLysValPheHisTyrGlnValLysIle 320
   |||||
Db 1156 ATGTACCTGAAGACTCGTTCTCAGATGCCCTACAAAGTCTTCCATTACCAAGTAAAGATT 1215

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QY 321 HisPheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGluIleSerLeuTyr 340
   |||||
Db 1216 CAITTTTCTGGACTGAGAGTGAACCCATACCAATCAGGCCTTTGAGATTCTCTGTAT 1275

QY 341 GlyThrValAlaGluSerGluAsnIleProPheThrThrLeuProGluValSerThrAsnLys 360
   |||||
Db 1276 GGCACCGTGGCCGAGAGTGAGAAACATCCCATCTGCTGCTGAAGTTTCCACAAATAAG 1335

QY 361 ThrTyrSerPheLeuIleTyrThrGluValAspIleGlyLeuLeuMetLeuLysLeu 380
   |||||
Db 1336 ACCATCTCTTCTTAATTTACACAGAGGTAGATATTGGAGAACTACTCATGTTGAAGCTC 1395

QY 381 LysTrpLysSerAspSerTyrPheSerTrpSerAspTrpSerProGlyPheAla 400
   |||||
Db 1396 AAATGGAAGATGATTCATCTTAGCTGGTCAGACTGGTGGAGAGTCCCGGCTTCGCC 1455

QY 401 IleGlnLysIleArgValLysAlaGlyGluThrGlnLysLysValIlePheCysSerArg 420
   |||||
Db 1456 ATTCAGAAATCAGAGTAAAGCAGCAGAGACTCAGAAAAAGGTGATCTTCTCTTAGG 1515

QY 421 GluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHisAsp 440
   |||||
Db 1516 GAGAAAGTGTCTCATTTGAGAAAGAAAGGACCCCTGCGGTATTGTGAATGCCATGAC 1575

QY 441 LysSerLeuAsnLysLysSerGly 448
   |||||
Db 1576 AAGTCTCTGAATAAGAAGTCAGGC 1599

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RESULT 3

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US-10-403-902A-13
; Sequence 13, Application US/10403902A
; Publication No. US20030224418A1
; GENERAL INFORMATION:
; APPLICANT: Braun, Andreas
; APPLICANT: Bansal, Aruna
; APPLICANT: Kleyn, Patrick
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND THEIR USE
; FILE REFERENCE: 24736-2048B
; CURRENT APPLICATION NUMBER: US/10/403,902A
; PRIOR FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: 09/802,640
; PRIOR FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 3549
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (175)...(1602)
; OTHER INFORMATION: Nucleotide sequence encoding lipoprotein lipase
; OTHER INFORMATION: (LPL)
US-10-403-902A-13

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Alignment Scores:

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Pred. No.: 5,18e-277 Length: 3549
Score: 2385.00 Matches: 448
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

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US-10-019-341-3 (1-448) x US-10-403-902A-13 (1-3549)

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QY 1 AlaAspGlnArgAspPheIleAspIleGluSerLysPheAlaLeuArgThrProGlu 20
   |||||
Db 256 GCCGACCAAGAGAGATTTATCGACATCGAAGTAAATTTGCCCTAAGGACCCCTGAA 315

QY 21 AspThrAlaGluAspThrCysHisLeuIleProGlyValAlaGluSerValAlaThrCys 40
   |||||

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Db 316 GACACAGCTGAGGACACTTGCCACCTCATTCCTCCGAGTAGCAGAGTCCGTGGCTACCTGT 375
Qy 41 HisPheAsnHisSerSerLysThrPheMetValIleHisGlyTrpThrValThrGlyMet 60
Db 376 CATTTCAATACACAGCAGCAAACTTCATGTGTATCCATGGCTGACGGTAACAGGAATG 435
Qy 61 TyrGluSerTrpValProLysLeuValAlaAlaLeuTyrLysArgGluProAspSerAsn 80
Db 436 TATGAGAGTTGGTGCCAAACTTGTGGCCGCTGTACAAAGAGAGAACCCAGACTCCCAAT 495
Qy 81 ValIleValValAspTrpLeuSerArgAlaGlnGluHisTyrProValSerAlaGlyTyr 100
Db 496 GTCAATTGTGTGGTGGCTGTCAAGGGCTCAGGAGCAATACCCAGTGTCCGGGGCTAC 555
Qy 101 ThrLysLeuValGlyGlnAspValAlaArgPheIleAsnTrpMetGluGluGluPheAsn 120
Db 556 ACCAAACTGGTGGGACAGAGTGGCCGGTTTATCACTGGATGGAGGAGGTTTAAAC 615
Qy 121 TyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeuGlyValAlaHisAlaGlyIle 140
Db 616 TACCTCTGGCAATGTCCATCTCTTGGGATACAGCTTGGAGCCCATGCTCTGGCATT 675
Qy 141 AlaGlySerLeuThrAsnLysLysValAsnAlaGlyIleThrGlyLeuAspProAlaGlyPro 160
Db 676 GCAGGAAGTCTGACCAATAAGAAAGTCAACAGAAATTACTGGCTCGATCCAGCTGGACCT 735
Qy 161 AsnPheGluTyrAlaGluAlaProSerArgLeuSerProAspAspAlaAspPheValAsp 180
Db 736 AACTTTGGATATGCAGAACCCCGAGTGTCTTCTCTGATGATGATGATGATGATGATGAT 795
Qy 181 ValLeuHisThrPheThrArgGlySerProGlyArgSerIleGlyIleGlnLysProVal 200
Db 796 GTCTTACACATTCACAGAGGCTCCCTGTGTGAAGTTCGAATCCAGAAACCCAGTT 855
Qy 201 GlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGlu 220
Db 856 GGGCATGTGTGACATTTACCGAATGAGGATCTTTTCAGCCAGGATGTAACTTGGAGAA 915
Qy 221 AlaIleArgValIleAlaGluArgGlyLeuGlyAspValAspGlnLeuValLysCysSer 240
Db 916 GCTATCCGCTGTATTCAGAGAGAGGACTTGGAGATGTGGACAGCTAGTGAAGTGTCTCC 975
Qy 241 HisGluArgSerIleHisLeuPheIleAspSerLeuLeuAsnGluLeuAsnProSerLys 260
Db 976 CACGAGCGCTCCATTCATCTCTTCATCGACTCTCTGTGAATGAAGAAATCCAGTAAG 1035
Qy 261 AlaTyrArgCysSerSerLysGluAlaPheGluLysGlyLeuCysLeuSerCysArgLys 280
Db 1036 GCCTACAGGTGCAGTTCACAGGAAGCCCTTTGAGAAAGGGCTCTGCTTGAGTTGTAGAA 1095
Qy 281 AsnArgCysAsnAsnLeuGlyTyrGluIleAsnLysValArgAlaLysArgSerSerLys 300
Db 1096 AACCGCTGCACAACTCTGGCTATGAGATCAATAAAGTCAGAGCCAAAGAGCAGCAAA 1155
Qy 301 MetTyrLeuLysThrArgSerGlnMetProTyrLysValPheHisTyrGlnValLysIle 320
Db 1156 ATGTACCTGAAGACTCGTCTCTCAGATGCCCTACAAAGCTTCCCAATACCAAGTAAGATT 1215
Qy 321 HisPheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGluIleSerLeuTyr 340
Db 1216 CATTTTCTGGGACTGAGAGTGAACCCATACCAATCAGGCTTTTGAGTTTCTCTGAT 1275
Qy 341 GlyThrValAlaGluSerGluAsnIleProPheThrLeuProGluValSerThrAsnLys 360
Db 1276 GGCACCGTGGCGGAGAGTGAACATCCATTCCTCTGCTGAAAGTTTCCACAAATAAG 1335
Qy 361 ThrTyrSerPheLeuIleTyrThrGluValAspIleGlyLeuLeuMetLeuLysLeu 380
Db 1336 ACCTACTCTCTTAAATTTACACAGAGTAGATATTGGAGAACTACTCATGTGTGAAGTCT 1395
Qy 381 LysTrpLysSerAspSerTyrPheSerTrpSerAspTrpTrpSerSerProGlyPheAla 400
Db 1396 AAATGGAAGAGTGAATTCATCTTTAGCTGGTCAGACTGCTGGAGCAGTCCCGGCTTCGCC 1455

Qy 401 IleGlnLysValIleArgValLysAlaGlyGluThrGlnLysLysValIlePheCysSerArg 420
Db 1456 ATTCAAGATCAGAGTAAAGCAGGAGACTCAGAAAAAGGTGATCTTCTGTCTTAGG 1515
Qy 421 GluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHisAsp 440
Db 1516 GAGAAAGTGTCTCTATTTGCAAGAAAGGACCTGCGGTATTTGTGAAATGCCATGAC 1575
Qy 441 LysSerLeuAsnLysLysSerGly 448
Db 1576 AAGTCTCTGAATAAGAGTCAGGC 1599
RESULT 4
US-10-755-889-99
; Sequence 99, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB
; TITLE OF INVENTION: PATHWAY
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 99
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-755-889-99
Alignment Scores:
Pred. No.: 5,18e-277 Length: 3549
Score: 2385.00 Matches: 448
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0
US-10-019-341-3 (1-448) x US-10-755-889-99 (1-3549)
Qy 1 AlaAspGlnArgArgAspPheIleAspIleGluSerLysPheAlaLeuArgThrProGlu 20
Db 256 GCCGACCAAGAAAGAGATTTTATCGACATCGAAAGTAAATTTGCCCTTAGGACCCCTGAA 315
Qy 21 AspThrAlaGluAspThrCysHisLeuIleProGlyValAlaGluSerValAlaThrCys 40
Db 316 GACACAGCTGAGGACACTTGCACCTCATTTCCCGAGTAGCAGAGTCCGTGGCTACCTGT 375
Qy 41 HisPheAsnHisSerSerLysThrPheMetValIleHisGlyTrpThrValThrGlyMet 60
Db 376 CATTTCAATACACAGCAGCAAACTTCATGTGTATCCATGGCTGACGGTAACAGGAATG 435
Qy 61 TyrGluSerTrpValProLysLeuValAlaAlaLeuTyrLysArgGluProAspSerAsn 80
Db 436 TATGAGAGTTGGTGGCCAAACTTGTGGCCGCTGTACAAAGAGAGAACCCAGACTCCCAAT 495
Qy 81 ValIleValValAspTrpLeuSerArgAlaGlnGluHisTyrProValSerAlaGlyTyr 100
Db 496 GTCAATTGTGTGGTGGCTGTCAAGGGCTCAGGAGCAATACCCAGTGTCCGGGGCTAC 555
Qy 101 ThrLysLeuValGlyGlnAspValAlaArgPheIleAsnTrpMetGluGluGluPheAsn 120
Db 556 ACCAAACTGGTGGGACAGGATGTGGCCGGTTTATCACTGGATGGAGGAGGTTTAAAC 615
Qy 121 TyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeuGlyValAlaHisAlaGlyIle 140
Db 616 TACCTCTGGCAATGTCCATCTCTTGGGATACAGCTTGGAGCCCATGCTCTGGCATT 675

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QY 141 AlaGlySerLeuThrAsnLysLysValAsnArgIleThrGlyLeuAspProAlaGlyPro 160
DB 676 GCAGGAAGTCTGACCAATAAGAAAGTCAACAGAAATTAATTCAGCTCGATCAGCTGACCT 735
QY 161 AsnPheGlyTyrAlaGluAlaProSerArgLeuSerProAspAspAlaAspPheValAsp 180
DB 736 AACTTTGAGTATGCAGAGCCCGAGTCGTCTTCTCTGATGATGATGATGATGATGATGATGAT 795
QY 181 ValLeuHisThrPheThrArgGlySerProGlyArgSerIleGlyIleGlnLysProVal 200
DB 796 GTCTTACACACATTACACAGAGGTCCTCTGTCGAAAGCATTTGGAATCCAGAAACAGATT 855
QY 201 GlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGlu 220
DB 856 GGGCATGTGTGACATTTACCGAATGGAGGTACTTTTCAGCCAGGATGTAACATTTGGAGAA 915
QY 221 AlaIleArgValIleAlaGluArgGlyLeuGlyAspValAspGlnLeuValLysCysSer 240
DB 916 GCTATCCCGGTGATTCGACAGAGAGGACTTGGAGATGTGGACAGCTAGTGAAGTGTCTCC 975
QY 241 HisGluArgSerIleHisLeuPheIleAspSerLeuLeuAsnGluGluAsnProSerLys 260
DB 976 CACGAGCGCTCCATTCATCTCTTCATCGACTCTCTGTTGAATGAAGAAATCCAAAGTAAG 1035
QY 261 AlaTyrArgCysSerSerLysGluAlaPheGluLysGlyLeuCysLeuSerCysArgLys 280
DB 1036 GCCTACAGGTGCAGTTCACAGAGCGCTTTCGAGAAAGGCTCTGTTGAGTTGTAGAAG 1095
QY 281 AsnArgCysAsnAsnLeuGlyTyrGluIleAsnLysValArgAlaLysArgSerLys 300
DB 1096 AACCGCTGCAACAATCTGGGTATGAGATCAATAAAGTCAGAGCCAAAGAAAGCAGCAAA 1155
QY 301 MetTyrLeuLysThrArgSerGlnMetProTyrLysValPheHisTyrGlnValLysIle 320
DB 1156 ATGTACCTGAGACTGTTCTTCAGATGCCCTTACAAAGTCTTCCATTACCAAGTAAGATT 1215
QY 321 HisPheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGluIleSerLeuTyr 340
DB 1216 CATTTTCTGGGACTGAGAGTGAAACCATACCAATCAGGCTTTGAGATTTCTCTGTAT 1275
QY 341 GlyThrValAlaGluSerGluAsnIleProPheThrLeuProGluValSerThrAsnLys 360
DB 1276 GGCACCTGCGCGAGAGTGAGAAATCCATCTCTGCTGAAAGTTTCACAAATAAG 1335
QY 361 ThrTyrSerPheLeuIleTyrThrGluValAspIleGlyGluLeuLeuMetLeuLysLeu 380
DB 1336 ACCTACTCTCTCTTAATTTACAGAGGTAGATATTGGAGAACTACTCATGTTGAAGCTC 1395
QY 381 LysTyrLysSerAspSerTyrPheSerTyrPheSerTyrPheSerTyrPheSerTyrPheAla 400
DB 1396 AAATGGAAGAGTGATTCATCTTATGCTGTGAGCTGTGGAGCAGTCCCGGCTTCGCC 1455
QY 401 IleGlnLysIleArgValLysAlaGlyGluThrGlnLysLysValIlePheCysSerArg 420
DB 1456 ATTGAGAGATCAGATGAAAGCAGGAGAGACTCAGAAAAAGGTGATCTTCTGTTCTAGG 1515
QY 421 GluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHisAsp 440
DB 1516 GAGAAAGTGTCTCATTTTGCAGAAAGGAAAGGCACCTCGCGTATTTGTGAATGCCATGAC 1575
QY 441 LysSerLeuAsnLysLysSerGly 448
DB 1576 AAGTCTCTGAATAAGAAGTCAGGC 1599
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RESULT 5

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US-10-116-802-28
; Sequence 28, Application US/10116802
; Publication No. US20030065157A1
; GENERAL INFORMATION:
; APPLICANT: Amy Lasek
; TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
; FILE REFERENCE: PA-0045 US
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; CURRENT APPLICATION NUMBER: US/10/116,802
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/281,593
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 519
; SOFTWARE: PERL Program
; SEQ ID NO 28
; LENGTH: 3635
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 3950154CB1
US-10-116-802-28
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Alignment Scores:

Pred. No.:	3,78e-276	Length:	3635
Score:	2378.00	Matches:	447
Percent Similarity:	100.00%	Conservative:	1
Best local Similarity:	99.78%	Mismatches:	0
Query Match:	99.71%	Indels:	0
DB:	14	Gaps:	0

US-10-019-341-3 (1-448) x US-10-116-802-28 (1-3635)

QY	1	AlaAspGlnArgArgAspPheIleAspIleGluSerLysPheAlaLeuArgThrProGlu	20
DB	331	GCCGACCACAAAGAGAGATTTTATCGACATCGAAGTAATTTGCCCTTAAGACCCCTGAA	390
QY	21	AspThrAlaGluAspThrCysHisLeuIleProGlyValAlaGluSerValAlaThrCys	40
DB	391	GACACAGCTGAGGACACTTGCACCTCATTCCTCCGAGTAGCAGAGTCGCTGGCTACCTGT	450
QY	41	HisPheAsnHisSerSerLysThrPheMetValIleHisGlyTyrThrValThrGlyMet	60
DB	451	CATTTCATCACACAGACCAAAACCTTCATGTGTATCAATGGCTGGACGGTAACAGGAATG	510
QY	61	TyrGluSerTrpValProLysLeuValAlaAlaLeuTyrLysArgGluProAspSerAsn	80
DB	511	TATGAGAGTTGGGTGCCAAACCTTGTGCGCCCTGTACAGAGAGAACCCAGATCCCAAT	570
QY	81	ValIleValIleAspTrpLeuSerArgAlaGlnGluHisTyrProValSerAlaGlyTyr	100
DB	571	GTCAATGTGTGGACTGGCTGTACGGGCTCAGGAGCATTTACCAGTGTCGCGGCTAC	630
QY	101	ThrLysLeuValGlyGlnAspValAlaArgPheIleAsnTrpMetGluGluGluPheAsn	120
DB	631	ACCAACTGTGGGACAGGATGTGGCCGGTTTATCAACTGGATGGAGAGGAATTTAAC	690
QY	121	TyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeuGlyAlaHisAlaGlyIle	140
DB	691	TACCTCTGGACAATGTCCATCTCTTGGGATACAGCCTTGGAGCCCATGTCTGTGGCAT	750
QY	141	AlaGlySerLeuThrAsnLysLysValAsnArgIleThrGlyLeuAspProAlaGlyPro	160
DB	751	GCAGGAAGTCTGACCAATAAGAAAGTCAACAGAAATTAATTCAGCTCCAGTCCAGT	810
QY	161	AsnPheGluTyrAlaGluAlaProSerArgLeuSerProAspAspAlaAspPheValAsp	180
DB	811	AACTTTGATGTACAGAGCCCGAGTCGTCTTCTCTGATGATGATGATGATGATGATGATGAT	870
QY	181	ValLeuHisThrPheThrArgGlySerProGlyValArgSerIleGlyIleGlnLysProVal	200
DB	871	GTCTTACACACATTCACAGAGGTCCTCTGTCGAAAGCATTTGGAATCCAGAAACAGTT	930
QY	201	GlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGlu	220
DB	931	GGGCATGTTGACATTTTACCCGGAATGAGGAGTACTTTTCAGCCAGGATGTAACATTTG	990
QY	221	AlaIleArgValIleAlaGluArgGlyLeuGlyAspValAspGlnLeuValLysCysSer	240
DB	991	GCTATCCCGCTGATTCAGAGAGAGACTTGGAGATGTGGACAGTGTAGTGAAGTGTCTCC	1050

QY	241	HisGluArgSerIleHisLeuPheIleAspSerLeuLeuAsnGluLeuAsnProSerLys	260
DB	1051	CACGAGCGCTCCATTCATCTCTTCATCGACTCTCTGTGAATGAAGAAAAATCCAAAGTAAG	1110
QY	261	AlaTyrArgCysSerSerLysGluAlaPheGluLysGlyLeuCysLeuSerCysArgLys	280
DB	1111	GCCTACAGGTGCAGTTCCTCAAGGAAGCCTTTGAGAAAGGGCTCTGCTTGAGTGTGAGAAAG	1170
QY	281	AsnArgCysAsnAsnLeuGlyTyrGluIleAsnLysValArgAlaLysArgSerSerLys	300
DB	1171	AACCGCTGCACCAATCTGGGCTATGAGATCAATAAAGTCAGAGCCAAAGAGCAGCAAA	1230
QY	301	MetTyrLeuLysThrArgSerGlnMetProTyrLysValPheHisTyrGlnValLysIle	320
DB	1231	ATGTACCTGAAGACTCGTTCTCAGATGCCCTACAAAGTCTTCCATTACCAAGTAAGATT	1290
QY	321	HisPheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGluIleSerLeuTyr	340
DB	1291	CATTTTCTGGGACTGAGAGTGAACCCATACCAATCAGGCCCTTTGAGATTCTCTGTAT	1350
QY	341	GlyTyrSerPheLeuIleTyrThrGluValAspIleGlyGluLeuLeuMetLeuLysLeu	360
DB	1351	GGCACCGTGGCGGAGAGTGAGACATCCCATTCATCTGCTGAGGTTTCCACAAATAAG	1410
QY	361	ThrTyrSerPheLeuIleTyrThrGluValAspIleGlyGluLeuLeuMetLeuLysLeu	380
DB	1411	ACCTACTCTCTCTAAATTTACACAGAGGTAGATATTGAGAACTACTCATGTGTGAAGCTC	1470
QY	381	LysTyrLysSerAspSerTyrPheSerTyrSerAspTyrTyrSerSerProGlyPheAla	400
DB	1471	AAATGGAAGAGTGATTCATATCTTTAGCTGGTCAGACTGGTGAGCAGCTCCCGCTTCGCC	1530
QY	401	IleGlnLysIleArgValLysAlaGlyGluThrGlnLysLysValIlePheCysSerArg	420
DB	1531	ATTCAGAGATCAGAGTAAACAGCAGAGAGACTCAGAAAAAGGTGATCTTCTGTCTAGG	1590
QY	421	GluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHisAsp	440
DB	1591	GAGAAAGTGCTCTCAATTTGCAGAAAGGAAAGGACCTGCGGTATTTGTGAAATGCCATGAC	1650
QY	441	LysSerLeuAsnLysLysSerGly	448
DB	1651	AAGTCTCTGAATAAGAAAGTCAGGC	1674
RESULT 6			
US-09-971-392-107			
; Sequence 107, Application US/09971392			
; Publication No. US20030134283A1			
; GENERAL INFORMATION:			
; APPLICANT: Peterson, David P.			
; APPLICANT: Pearson, Cecelia I.			
; APPLICANT: Cocks, Benjamin G.			
; TITLE OF INVENTION: GENES REGULATED IN DENDRITIC CELL DIFFERENTIATION			
; FILE REFERENCE: PA-0029 US			
; CURRENT APPLICATION NUMBER: US/09/971,392			
; CURRENT FILING DATE: 2001-10-03			
; PRIOR APPLICATION NUMBER: 60/237,652			
; PRIOR FILING DATE: 2000-10-03			
; NUMBER OF SEQ ID NOS: 260			
; SOFTWARE: PERL Program			
; SEQ ID NO 107			
; LENGTH: 4075			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: misc_feature			
; OTHER INFORMATION: Template ID: 049457.6			
US-09-971-392-107			
Alignment Scores:			
Pred. No.:	2,41e-275	Length:	4075
Score:	2372.00	Matches:	448
Percent Similarity:	99.78%	Conservative:	0

Best Local Similarity:	99.78%	Mismatches:	0
Query Match:	99.45%	Indels:	1
DB:	10	Gaps:	0
US-10-019-341-3 (1-448) x US-09-971-392-107 (1-4075)			
QY	1	AlaAspGlnArgArgAspPheIleAspIleGluSerLysPheAlaLeuArgThrProGlu	20
DB	750	GCCGACCAAGAGAGATTTTATCGACATCGAAGATAAATTGCGCTTAAGGACCCCTGAA	809
QY	21	AspThrAlaGluAspThrCysHisLeuIleProGlyValAlaGluSerValAlaThrCys	40
DB	810	GACACAGCTGAGGACACTTCCCACTCATTTCCCGAGTAGCAGAGTCGCTGGCTACCTCTGT	869
QY	41	HisPheAsnHisSerSerLysThrPheMetValIleHisGlyTyrThrValThrGlyMet	60
DB	870	CATTTCATACACAGCAGCAAAACCTTTCATGCTGATTCATGCTGGACGGTAACAGGAATG	929
QY	61	TyrGluSerTyrProLysLeuValAlaLeuTyrLysArgGluProAspSerAsn	80
DB	930	TATGAGAGTTGGTGCCAAACTTGTGGCCGCTGTACAAGAGAGAACCCAGACTCCCAAT	989
QY	81	ValIleValValAspTyrLeuSerArgAlaGlnGluHisTyrProValSerAlaGlyTyr	100
DB	990	GTCAATTTGTGTGGACTGGCTGTCTACGGGCTCAGGAGCAATTAACCCAGTGTCCGCGGCTAC	1049
QY	101	ThrLysLeuValGlyGlnAspValAlaArgPheIleAsnTyrMetGluGluGluPheAsn	120
DB	1050	ACCAAACTGGTGGGACAGATGTGGCCGGTTTATCACTGGATGGAGGAGAGTTTAAAC	1109
QY	121	TyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeuGlyAlaHisAlaAlaGlyIle	140
DB	1110	TACCTCTGGCAATGTCCATCTCTTGGGATACAGCCTTGGAGCCCATGCTGTGGCATT	1169
QY	141	AlaGlySerLeuThrAsnLysLysValAsnArgIleThrGlyLeuAspProAlaGlyPro	160
DB	1170	GCAGGAAGTCTGACCAATAAGAAAGTCAACAGAAATTACTGGCCTCGATCCAGCTGGACCT	1229
QY	161	AsnPheGluTyrAlaGluAlaProSerArgLeuSerProAspAspAlaAspPheValAsp	180
DB	1230	AACTTTGAGTATGCAAGAGCCCGAGTGTCTTTCTCTGATGATGCAGATTTGTAGAC	1289
QY	181	ValLeuHisThrPheThrArgGlySerProGlyArgSerIleGlyIleGlnLysProVal	200
DB	1290	GTCTTACACACATTCACAGAGGGTCCCTCGTGGAAAGCATTTGGAATCCAGAAACCAAGT	1349
QY	201	GlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGlu	220
DB	1350	GGGCATGTTGACATTTACCCGAATGGAGGTACTTTTCAGCCAGGATGTAAACATTGGAGAA	1409
QY	221	AlaIleArgValIleAlaGluArgGlyLeuGlyAspValAspGlnLeuValLysCysSer	240
DB	1410	GCATCCGCGTGAATTCACAGAGAGACTTGGAGATGTGGACAGCTAGTGAAGTGTCTCC	1469
QY	241	HisGluArgSerIleHisLeuPheIleAspSerLeuLeuAsnGluGlnProSerLys	260
DB	1470	CACGAGCGCTCCATTCATCTCTCATCGACTCTCTGTGAATGAAGAAATCCAAAGTAAG	1529
QY	261	AlaTyrArgCysSerSerLysGluAlaPheGluLysGlyLeuCysLeuSerCysArgLys	280
DB	1530	GCCTACAGGTGCGATTCCCAAGGAGCCTTTGAGAAAGGGCTCTGCTTGTAGTGTAGAAAG	1589
QY	281	AsnArgCysAsnAsnLeuGlyTyrGluIleAsnLysValArgAlaLysArgSerSerLys	300
DB	1590	AACCGCTGCACCAATCTGGGCTATGAGATCAATAAAGTCAGAGCCAAAGAGCAGCAAA	1649
QY	301	MetTyrLeuLysThrArgSerGlnMetProTyrLysValPheHisTyrGlnValLysIle	320
DB	1650	ATGTACCTGAAGACTCGTTCTCAGATGCCCTACAAAGCTTCCATTACCAAGTAAGATT	1709
QY	321	HisPheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGluIleSerLeuTyr	340
DB	1710	CATTTTCTGGGACTGAGAGTGAACCCATACCAATCAGGCTTTGAGATTCTCTGTAT	1769

QY 341 GlyThrValAlaGluSerGluAsnIleProPheThrLeuProGluValSerThrAsnLys 360
Db 1770 GGCACCGTGGCCGAGAGTGGAGACATCCCATTCCTGCTGAGGTTTCCCAATAAG 1829
QY 361 ThrTyrSerPheLeuIleTyrGluValAlaAspIleGlyGluLeuLeuMetLeuLysLeu 380
Db 1830 ACCTACTCTCTCTAATTTACACAGAGGTAGATATTGGAGAACTACTCATGTTGAAGCTC 1889
QY 381 LysTrpLysSerAspSerTyrPheSerTrpSerAspTrpTrpSerSerProGlyPheAla 400
Db 1890 AAATGGAAGAGTATTCATCTTTAGCTGGTCCAGACTGGTGAGCAGTCCCGCTTCGCC 1949
QY 401 Ile-GlnLysIleArgValLysAlaGlyGluThrGlnLysLysValIlePheCysSerTr 420
Db 1950 ATTGCAGAGATCAGNGTAAAGCAGGAGAGACTCAGAAAAGGTGATCTTCTGTCTAG 2009
QY 420 gGluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHisAs 440
Db 2010 GGAGAAAGTGTCTCATTTGCAGAAAGGAAAGGCACCTCGGTATTGTGAAATGCCATGA 2069
QY 440 pLysSerLeuAsnLysLysSerGly 448
Db 2070 CAAGTCTCTGAAATAAGAGTCAGGC 2094

RESULT 7

US-10-388-934-188
; Sequence 188, Application US/10388934
; Publication No. US20040005547A1
; GENERAL INFORMATION:
; APPLICANT: Boess, Franziska
; APPLICANT: Suter-Dick, Laura
; APPLICANT: Wolf, Detlef
; TITLE OF INVENTION: BIOMARKERS AND EXPRESSION PROFILES FOR TOXICOLOGY
; FILE REFERENCE: 21199
; CURRENT APPLICATION NUMBER: US/10/388,934
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 02005336.9
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 02015657.6
; PRIOR FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 862
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 188
; LENGTH: 3617
; TYPE: DNA
; ORGANISM: Rattus norvegicus (No. US20040005547A1way rat)
US-10-388-934-188

Alignment Scores:
Pred. No.: 6,41e-259 Length: 3617
Score: 2235.50 Matches: 416
Percent Similarity: 96.65% Conservative: 17
Best Local Similarity: 92.86% Mismatches: 14
Query Match: 93.73% Indels: 1
DB: 16 Gaps: 1

US-10-019-341-3 (1-448) x US-10-388-934-188 (1-3617)

QY 1 AlaAspGlnArgArgAspPheIleAspIleGluSerLysPheAlaLeuArgThrProGlu 20
Db 256 GCAGACGGGGGAAGAGATTCTCAGACATCGAAAGTAAATTTGCCCTAAGGACCCCTGAA 315
QY 21 AspThrAlaGluAspThrCysHisLeuIleProGlyValAlaGluSerValAlaThrCys 40
Db 316 GACACAGCTGAGGACATCTGTCTATCTGATTCCTGGATTAGCAGACTCTGTGTCTAACTGC 375
QY 41 HisPheAsnHisSerSerLysThrPheMetValIleHisGlyTrpThrValThrGlyMet 60
Db 376 CATTTCNACCACAGCAGCAAAACCTTTGTGGTATCCATGGATGGACGGTGACAGGAATG 435
QY 61 TyrGluSerTrpValProLysLeuValAlaAlaLeuTyrLysArgGluProAspSerAsn 80

Db 436 TATGAGAGTTGGTGGTCCCAAACTTGTGGCTGCCCTATACAAAAGAGAACCTGACTCCAAT 495
QY 81 ValIleValValAspTrpLeuSerArgAlaGlnGluHisTyrProValSerAlaGlyTyr 100
Db 496 GTCAITTTAGTAGACTGGTTGTATCGGGCCGAGCAACATTTCCAGTGTCTCGCGGTAT 555
QY 101 ThrLysLeuValGlyGlnAspValAlaArgPheIleAsnTrpMetGluGluGluPheAsn 120
Db 556 ACCAAGCTGTGGGAAATGATGTGCCAGGTTTCATCACTGCTGCGAGGAGAAATTTAAC 615
QY 121 TyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeuGlyAlaHisAlaAlaGlyIle 140
Db 616 TACCCCTTAGACAATGTCCACTTCTAGGGTACAGTCTTTGGAGCCCATCTGCTGGCGTG 675
QY 141 AlaGlySerLeuThrAsnLysLysValAsnArgIleThrGlyLeuAspProAlaGlyPro 160
Db 676 GCAGGAAGTCTGACCCACACAGNAGGTCAATAGATTACTGGCTTGGATCCAGCTGGGCT 735
QY 161 AsnPheGluTyrAlaGluAlaProSerArgLeuSerProAspAspAlaAspPheValAsp 180
Db 736 AACTTTGAGTATGCAGAAAGCCCTAGTCGCCCTTTCTCTGATGATGCGGATTTCTGAT 795
QY 181 ValLeuHisThrPheThrArgGlySerProGlyArgSerIleGlyIleGlnLysProVal 200
Db 796 GTCTTTACACACATTTTACCAGGGGTCGCTCGTCTGAGTATTGGGATCCAGAAACAGTA 855
QY 201 GlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGlu 220
Db 856 GGGCATGTTGATATTTATCCCAATGGAGGCATTTCCAGCCAGGATGCAACATTCGAGAA 915
QY 221 AlaIleArgValIleAlaGluAlaGluArgGlyLeuGlyAspValAspGlnLysCysSer 240
Db 916 GCCATTCTGTTAAATGCAGAGAGGGCTTCGAGATGTGGACCACTGCTGATGCTCG 975
QY 241 HisGluArgSerIleHisLeuPheIleAspSerLeuLeuAsnGluGluAsnProSerLys 260
Db 976 CACGAGCGCTCCATCCATCTCTTATTGACTCCCTGCTGAAATGAAGAAACCCAGCAAG 1035
QY 261 AlaTyrArgCysSerSerLysGluAlaPheGluLysGlyLeuCysLeuSerCysArgLys 280
Db 1036 GCATACAGTGCATTTCCAGGAGGCTTTGAGAAAGGCTCTGCTGAGTTGCAGAAAG 1095
QY 281 AsnArgCysAsnAsnLeuGlyTyrGluIleAsnLysValArgAlaLysArgSerSerLys 300
Db 1096 AATCGCTGTAACAACGTGGGCTATGAGATCAACAAGGTTCAGAGCCAGAGAGCAGTAAG 1155
QY 301 MetTyrLeuLysThrArgSerGlnMetProTyrLysValPheHisTyrGlnValLysIle 320
Db 1156 ATGTACCTGAAGACTCGCTCTCAGATGCCCTTACAAAGTATTTCATTACCAAGTCAAGATT 1215
QY 321 HisPheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGluIleSerLeuTyr 340
Db 1216 CACTTTTCTGGAAGTGCATGAGATGACAGCAACCAACAGGCTTCGAGATTCTCTGTAT 1275
QY 341 GlyThrValAlaGluSerGluAsnIleProPheThrLeuProGluValSerThrAsnLys 360
Db 1276 GGCACAGTGGCTGAAAGTGAGAACATTTCCCTTCACCTGCGGAGGTCGCCACAAATAA 1335
QY 361 ThrTyrSerPheLeuIleTyrThrGluValAspIleGlyGlnLeuLeuMetLeuLysLeu 380
Db 1336 ACCTACTCTCTTCTGTATTTACCGGAGGTGAGATCGGGGAATTTGCTGATGATCAAGCTT 1395
QY 381 LysTrpLysSerAspSerTyrPheSerTrpSerAspTrpTrpSerSerProGlyPheAla 400
Db 1396 AAGTGGAGAGAACACTCTTACTTCCGCTGGTCAAGCTGGTGAGCAGTCCAGCTTTGTC 1455
QY 401 IleGlnLysIleArgValLysAlaGlyGluThrGlnLysLysValIlePheCysSerArg 420
Db 1456 ATCGAAGATCCGAGTGAAGCCGAGAGACTCAGAAAAGGTCTATCTTCTGTGCCAGG 1515
QY 421 GluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHisAsp 440
Db 1516 GAGAAAGTTTCTCATCTGCAGAAAGGAGGACGCTGCAGTGTTCGTGAAATGCCATGAC 1575

QY 441 LysSerLeuAsnLysLysSerGly 448

Db 1576 AAGTCTCTG--AAGAAAGTCGGC 1596

RESULT 8

US-10-128-449A-7

Sequence 7, Application US/10128449A

Publication No. US20030108538A1

GENERAL INFORMATION:

APPLICANT: Jaye, Michael C.
Doan, Kim-Anh T.
Krawiec, John A.
Lynch, Kevin J.
Amin, Dilip V.
South, Victoria J.

TITLE OF INVENTION: LIG POLYPEPTIDES OF THE TRIACYLGLYCEROL
LIPASE FAMILY, AND COMPOSITIONS AND METHODS FOR THEIR USE
IN ENZYMIC HYDROLYSIS, AND PROTEIN AND GENE THERAPIES

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESS: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Rd. 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/128,449A

FILING DATE: 23-Apr-2002

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Fehner Ph.D., Paul F.
REGISTRATION NUMBER: 35,135

REFERENCE/DOCKET NUMBER: A2582-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (610)454-3839

TELEFAX: (610)454-3808

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 2565 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 252..1754

SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-10-128-449A-7

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

3,26e-129

1161.00

69.16%

48.98%

48.68%

15

Length:

Matches:

Conservative:

Mismatches:

Indels:

Gaps:

2565

216

89

118

18

6

US-10-019-341-3 (1-448) x US-10-128-449A-7 (1-2565)

QY 13 LysPheAlaLeuArgThrProGluAspThrAlaGluAspThrCysHisLeuLeuProGly 32

Db 399 AGGTTTAACCTCGCACCTCCAGAGGCCCGGACGATGAGGATGCTACCTCTCGTCGGC 458

QY 33 ValAlaGluSerValAlaThrCysHisPheAsnHisSerSerLysThrPheMetValile 52

Db 459 CACAGCCAGCCCTAGAGAGCTGCAGTTTCAACATGACAGCTAAACCTTTTTCATCAT 518

QY 53 HisGlyTrpThrValThrGlyMetTyrGluSerTrpValProLysLeuValAlaLeu 72

Db 519 CACGATGGACGATGACGGTATCTTTGAAAACTGGCTGCACAACTCGTGTACGCCCTG 578

QY 73 TyrLysArgGluProAspSerAsnValIleValValAspTrpLeuSerArgAlaGlnGlu 92

Db 579 CACACAAGAGAGAAAGACGCCAATGTAGTTGTGGTTGACTGGCTCCCTCCGCCCCACG 638

QY 93 HisTyrProValSerAlaGlyTyrThrLysLeuValGlyGlnAspValAlaArgPheIle 112

Db 639 CTTTACACGGATCGGTCATTAATACCCAGGGTGGTGACACAGCAITGCCAGGATGTC 698

QY 113 AsnTrpMetGluGluGluPheAsnTyrProLeuAspAsnValHisLeuLeuGlyTyrSer 132

Db 699 GACTGGCTGCAGAGAGAGGACGATTTTCTTCGGGAATGTCACATTCATCGGTACAGC 758

QY 133 LeuGlyAlaHisAlaAlaGlyIleAlaGlySerLeuThrAsnLysLysValAsnArgIle 152

Db 759 CTCGAGCGCACGTGGCGCGGTATGTCAGGCACTTCGTGAAAGGAACCGTGGCGCGAATC 818

QY 153 ThrGlyLeuAspProAlaGlyProAsnPheGluTyrAlaGluAlaProSerArgLeuSer 172

Db 819 ACAGGTTTGGATCCTCGCGGCCCATGTTTGAGGGGCCGACATCCACAGAGGCTCTCT 878

QY 173 ProAspAlaAspPheValAspValLeuHisThrPheThrArgGlySerProGlyArg 192

Db 879 CCGAGCATGACGATTTTGTGGATGCTCTCCACACCTACACGGGT--TCCTTCGGCTTG 935

QY 193 SerIleGlyIleGlnLysProValGlyHisValAspIleTyrProAsnGlyThrPhe 212

Db 936 AGCATTTGTATTTCAGATGCTGTGGGCCACATGATCATCTACCCCAATGGGGGTGACTTC 995

QY 213 GlnProGlyCysAsnIleGlyGluAlaIleArgValIleAlaGluArgGlyLeuGlyAsp 232

Db 996 CAGCCAGGCTGTGGACTCAACGATGCTTTGGGATCAATTGCA-----TATGGAACA 1046

QY 233 ValAspGlnLeuValLysCysSerHisGluArgSerIleHisLeuPheIleAspSerLeu 252

Db 1047 ATCAGAGAGTGTAAATGTGAGCATGAGCGCGCTCCACCTCTTTGTGACTCTCTG 1106

QY 253 LeuAsnGluGluAsnProSerLysAlaTyrArgCysSerSerLysGluAlaPheGluLys 272

Db 1107 GTGAATCAGGCAACGCCGAGTTTTCCTTCCAGTGCATCTCAATCGCTTCAAAAAG 1166

QY 273 GlyLeuCysLeuSerCysArgLysAsnArgCysAsnAsnLeuGlyTyrGluIleAsnLys 292

Db 1167 GGGATCTGTCTGAGCTGCCGCAAGAACCGTTGTAATAGCATTTGGCTACATGCCAAGAAA 1226

QY 293 ValArgAlaLysArgSerSerLysMetTyrLeuLysThrArgSerGlnMetProTyrLys 312

Db 1227 ATGAGGAACAGAGGAGGACAAATGTACTTAAACCCCGGCGGCGCATGCTTTTCAGA 1286

QY 313 ValPheHisTyrGlnValLysIleHisPheSerGlyThrGluSerGluThrHisThrAsn 332

Db 1287 GTTTACCATTTATCAGATGAATAATCCATGCTTCAGTTACAAGAACATGGGAGAAATGAG 1346

QY 333 GlnAlaPheGluIleSerLeuTyrThrValAlaGluSerGluAsnIleProPheThr 352

Db 1347 CCACCTTTTACGTCACCTTTTATGGCACTAATGCAGATTTCCAGACTCTGCCACTGGAA 1406

QY 353 LeuProGlu---ValSerThrAsnLysThrTyrSerPheLeuIleTyrThrGluValAsp 371

Db 1407 ATAGTCGAGCGGATCGAGCAGATGCCACCAACACCTTCTCTGCTTACACCGAGGAGAC 1466

QY 372 IleGlyGluLeuLeuMetLeuLysLeuLysTrpLysSerAspSerTyrPheSerTrpSer 391

Db 1467 TTGGAGACCTCTTTGAAGATCCAGCTCACCTGGGAGGGGGCTCTCAG--TCTTGTATC 1523

QY 392 AspTrpTrpSer-----SerProGly-----Phe 399

Db 1524 AACCTGTGGAAGGAGTTTCGACGTACTCTCTCAACCCCGCAACCCCGGACGGAGCTG 1583

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QY 400 AlaileGlnLysIleArgValLysAlaGluThrGlnLysLysValIlePheCysSer 419
Db 1584 AATATCAGCGCATCGGGTGAAGTCTGGGAAACCCAGCGGAACATGACATTTGTACA 1643
QY 420 ArgGluLysValSerHisLysGlnLysGlyLysAlaProAlaPheValLysCysHis 439
Db 1644 GAGACCTCGAGAACACACCATATCCCGAGCGGAGCTCTGGTTTCGCAAGTGTGCG 1703
QY 440 Asp 440
Db 1704 GAT 1706

RESULT 9
US-10-354-358-45
; Sequence 45, Application US/10354358
; Publication No. US20030157082A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Hunter, John Joseph
; APPLICANT: Macbeth, Kyle J.
; APPLICANT: Tsai, Fong-Ying
; APPLICANT: Lesoon, Andrea
; APPLICANT: Lightcap, Eric S.
; APPLICANT: Williamson, Mark
; APPLICANT: Rudolph-Owen, Laura A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CANCER USING 140, 1470, 1686, 2089, 2427, 3702, 5891, 6428,
; TITLE OF INVENTION: 7181, 7660, 25641, 69583, 49863, 8897, 1682, 17667, 9235,
; TITLE OF INVENTION: 3703, 14171, 10359, 1660, 1450, 18894, 2088, 32427, 2160,
; TITLE OF INVENTION: 9252, 9389, 1642, 85269, 10297, 1584, 9525, 14124, 4469,
; TITLE OF INVENTION: 8990, 2100, 9288, 64698, 10480, 20893, 33230, 1586, 9943,
; TITLE OF INVENTION: 16334, 68862, 9011, 14031, 6178, 21225, 1420, 32236, 2099,
; TITLE OF INVENTION: 2150, 26583, 2784, 8941, 9811, 27444, 50566 OR 66428 MOLECULES
; FILE REFERENCE: MPI02-020P1RNM0NM
; CURRENT APPLICATION NUMBER: US/10/354,358
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/353,600
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 60/364,517
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/371,075
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/371,507
; PRIOR FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: US 60/372,984
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/374,194
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/382,995
; PRIOR FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 60/385,023
; PRIOR FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: US 60/388,853
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/389,395
; PRIOR FILING DATE: 2002-06-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 3927
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (253)....(1755)
US-10-354-358-45

Alignment Scores:
Pred. No.: 6,42e-129 Length: 3927
Score: 1161.00 Matches: 216
Percent Similarity: 69.16% Conservative: 89
Best Local Similarity: 48.98% Mismatches: 118

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Query Match: 48.68% Indels: 18
DB: 15 Gaps: 6
US-10-019-341-3 (1-448) x US-10-354-358-45 (1-3927)
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Db 400 AGGTTTAACTTCGCGACCTCCAGAGCCAGAGCATGAAGATGCTACCTCTCGTCGGC 459
QY 33 ValAlaGluSerValAlaThrCysHisPheAsnHisSerSerLysThrPheMetValIle 52
Db 460 CACAGCCAGCCCTTAGAAGACTGCAGTTTCAACATGACAGCTAAACCTTTTTCATCAT 519
QY 53 HisGlyTrpThrValThrGlyMetTyrGluSerTrpValProLysLeuValAlaLeu 72
Db 520 CACGGATGACGATGAGCGGTATCTTTGAAAACCTGGCTGCACAACTCTGTGTGAGCCCTG 579
QY 73 TyrLysArgGluProAspSerAsnValIleValValAspTrpLysLeuValAlaArgPheIle 112
Db 580 CACACAAGAGAGAAAGACGCCAATGTAGTTGTGTGACTGCTCCCTCGGCCACACAG 639
QY 93 HisTyrProValSerAlaGlyTyrThrLysLeuValGlyGlnAspValAlaArgPheIle 112
Db 640 CTTTACCGATGCGGTCAATATACCGGGTGGGACACAGCATTCGCCAGGATGCTC 699
QY 113 AsnTrpMetGluGluGluPheAsnTyrProLeuAspAsnValHisLeuLeuGlyTyrSer 132
Db 700 GACTGCTGTCAGAGACAGCATTTTCTCTCGGAATGTCACATTTGATTCGGCTACAGC 759
QY 133 LeuGlyAlaHisAlaAlaGlyIleAlaGlySerLeuThrAsnLysLysValAsnArgIle 152
Db 760 CTCGAGCGCACGTCGGCGGTATGACGAGCACTTCGTGAAAGGAACGCTGGCGCGAATC 819
QY 153 ThrGlyLeuAspProAlaGlyProAsnPheGluTyrAlaGluAlaProSerArgLeuSer 172
Db 820 ACAGGTTTGGATCTGCGCGGCCCATATGTTGAAGGGCCGACATCCACAAGAGGCTCTCT 879
QY 173 ProAspAlaAspPheValAspValLeuHisThrPheThrArgGlySerProGlyArg 192
Db 880 CCGGACGATGACGATTTTGTGATGTCCTCCACACCTACACGCGT--TCCTTCGGCTTG 936
QY 193 SerIleGlyIleGlnLysProValGlyHisValAspIleTyrProAsnGlyGlyThrPhe 212
Db 937 AGCATTTGTAATTCAGATGCTGTCGGCCACATTCACATCTACCCCAATGGGGTGACTTC 996
QY 213 GlnProGlyCysAsnIleGlyGluAlaIleArgValIleAlaGluArgGlyLeuGlyAsp 232
Db 997 CAGCCAGCTGTGACATCAGCATGTCTTGGGATCAATTGCA-----TATGGAACA 1047
QY 233 ValAspGlnLeuValLysCysSerHisGluArgSerIleHisLeuPheIleAspSerLeu 252
Db 1048 ATCAGAGGTGTGTAATAATGTGAGCATGAGCGCCGTCACCTCTTTTGTGATCTCTG 1107
QY 253 LeuAsnGluGlnAsnProSerLysAlaTyrArgCysSerSerLysGluAlaPheGluLys 272
Db 1108 GTGAATCAGACAACGCCAGTTTTCCTCCAGTGCATGACTCACTCAATCGCTTCAAAAAG 1167
QY 273 GlyLeuCysLeuSerCysArgLysAsnArgCysAsnAsnLeuGlyTyrGluIleAsnLys 292
Db 1168 GGGATCTGTGAGTGTGCCCAAGAACCGGTGTGAATAGCATTTGGCTACAATGCCAAGAA 1227
QY 293 ValArgAlaLysArgSerSerLysMetTyrLeuLysThrArgSerGlnMetProTyrLys 312
Db 1228 ATGAGGAACAAGAGGAACAGCAAAATGTACTTAAAAACCCGCGCAGGATGCTCTTTCAGA 1287
QY 313 ValPheHisTyrGlnValLysIleHisPheSerGlyThrGluSerGluThrHisThrAsn 332
Db 1288 GTTTACCATTTATCAGATGAATAATCCATGTCTTCAGTTTACAAGAACATCGGAGAAATTGAG 1347
QY 333 GlnAlaPheGluIleSerLeuTyrGlyThrValAlaGluSerGluAsnIleProPheThr 352
Db 1348 CCCACCTTTTACGTCAACCTTTTATGGCACTAATGTCAGATTCACGACTCTGCCACTGGAA 1407

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QY 353 LeuProGlu---ValSerThrAsnLysThrTyrSerPheLeuIleTyrThrGluValAsp 371
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 QY 372 IleGlyGluLeuMetLeuLysLeuLysLeuLysSerAspSerTyrPheSerTyrSer 391
 DB 1468 TTGGGAGACCTTTGAAGATCCAGCTCACCTGGGAGGGGGCTCTCAG---TCTTGGTAC 1524
 QY 392 AspTrpTrpSer-----SerProGly-----Phe 399
 DB 1525 AACCTGTGAAGAGATTTCGAGCTACCTGTCTCAACCCCGCAACCCGCGGAGGAGCTG 1584
 QY 400 AlaIleGlnLysIleArgValLysAlaGlyGluThrGlnLysLysValIlePheCysSer 419
 DB 1585 AATATCAGCGCATCGGGTGAAGTCTGGGAAACCCAGCGGAACCTGACATTTTGTACA 1644
 QY 420 ArgGlnLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHis 439
 DB 1645 GAAGACCTGGAACACCCAGCATATCCCGAGCGGGAGCTCTGGTTTCGCAAGTGTGG 1704
 QY 440 Asp 440
 DB 1705 GAT 1707
 DB
 RESULT 10
 US-10-172-118-1234
 ; Sequence 1234, Application US/10172118
 ; Publication No. US20030224374A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dai, Hongyue
 ; APPLICANT: He, Yudong
 ; APPLICANT: Linsley, Peter
 ; APPLICANT: Mao, Mao
 ; APPLICANT: Roberts, Chris
 ; APPLICANT: Van 't Veer, Laura
 ; APPLICANT: Van de Vijver, Marc
 ; APPLICANT: Bernards, Rene
 ; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
 ; FILE REFERENCE: 9301-175-999
 ; CURRENT APPLICATION NUMBER: US/10/172,118
 ; CURRENT FILING DATE: 2002-06-14
 ; PRIOR APPLICATION NUMBER: 60/380,770
 ; PRIOR FILING DATE: 2002-05-14
 ; NUMBER OF SEQ ID NOS: 2699
 ; SEQ ID NO 1234
 ; LENGTH: 3927
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; PUBLICATION INFORMATION:
 ; DATABASE ACCESSION NUMBER: NM_006033
 ; DATABASE ENTRY DATE: 2001-06-18
 US-10-172-118-1234
 Alignment Scores:
 Pred. No.: 6,42e-129 Length: 3927
 Score: 1161.00 Matches: 216
 Percent Similarity: 69.16% Conservative: 89
 Best Local Similarity: 48.98% Mismatches: 118
 Query Match: 48.68% Indels: 18
 DB: 15 Gaps: 6
 US-10-019-341-3 (1-448) x US-10-172-118-1234 (1-3927)
 QY 13 LysPheAlaLeuArgThrProGluAspThrAlaGluAspThrCysHisLeuIleProGly 32
 DB 400 AGGTTTAACTCCGCACCTCCAGGACCCAGAGATGAAGGATGCTACCTCTCGTGGC 459
 QY 33 ValAlaGluSerValAlaThrCysHisPheAsnHisSerSerLysThrPheMetValIle 52
 DB 460 CACAGCCAGCCCTTAGAAGACTGCGAGTTTCAACATGACAGCTAAACCTTTTCATATT 519
 QY 53 HisGlyTrpThrValThrGlyMetTyrGluSerTrpValProLysLeuValAlaLeu 72

DB 520 CACGGATGACGATGACGGGTATCTTTGAAAACTGGCTGCACAAACTCGTGTGTGACGCCCTG 579
 QY 73 TyrLysArgGluProAspSerAsnValIleValValAspTrpLeuSerArgAlaGlnGlu 92
 DB 580 CACAACAGAGAGAAAGACGCCAATGTAGTGTGTGTGCTGCTCCCTGTCGCCACACG 639
 QY 93 HisTyrProValSerAlaGlyTyrThrLysLeuValGlyGlnAspValAlaArgPheIle 112
 DB 640 CTTTACACGGATGCGGTCAATAATACACGGGTGTGGGACACAGCATTCGCCAGGATGCTC 699
 QY 113 AsnTrpMetGluGluGluPheAsnTyrProLeuAspAsnValHisLeuLysLeuGlyTyrSer 132
 DB 700 GACTGGCTGACGAGAAAGACGATTTTCTCTCGGGAATGCTCCATCTGATCGGTACACG 759
 QY 133 LeuGlyAlaHisAlaAlaGlyIleAlaGlySerLeuThrAsnLysLysValAsnArgIle 152
 DB 760 CTCGAGGCGCATCGGCCGGGTATGCAGGCAACTTCGTGAAGGAACGCGTGGCGCGAATC 819
 QY 153 ThrGlyLeuAspProAlaGlyProAsnPheGluTyrAlaGluAlaProSerArgLeuSer 172
 DB 820 ACAGTTTGGATCTCTCGCGGCCCATGTTTGAAGGGCGGCACATCCACAAGAGGCTCTCT 879
 QY 173 ProAspAlaAspPheValAspValLeuHisThrPheThrArgGlySerProGlyArg 192
 DB 880 CCGGACGATGACGATTTTGTGGATGCTCTCCACACTACACGCGT---TCTTCCGCTTG 936
 QY 193 SerIleGlyIleGlnLysProValGlyHisValAspIleTyrProAsnGlyGlyThrPhe 212
 DB 937 AGCATTTGGTATTTCAGATGCTGTGGCCACATGACATCTACCCCAATGGGGGTGACTTC 996
 QY 213 GlnProGlyCysAsnIleGlyGluAlaIleArgValIleAlaGluArgGlyLeuGlyAsp 232
 DB 997 CAGCCAGGCTGTGGACTCAACGATGCTTGGGATCAATTGCA-----TATGGAAACA 1047
 QY 233 ValAspGlnLeuValLysCysSerHisGluArgSerIleHisLeuPheIleAspSerLeu 252
 DB 1048 ATCAGAGAGTGTGTAATAATGTGAGTGGCGGCGGTCCACCTCTTTGTGACTCTCTG 1107
 QY 253 LeuAsnGluLysAsnProSerLysAlaTyrArgCysSerSerLysGluAlaPheGluLys 272
 DB 1108 GTGAATCAGGACAAGCGGAGTTTTCCTTCCAGTGACTGACTCCCAATCGTTTCAAAAAG 1167
 QY 273 GlyLeuCysLeuSerCysArgLysAsnArgCysAsnAsnLeuGlyTyrGluIleAsnLys 292
 DB 1168 GGGATCTGTGAGCTGCCGCAAGACCGTGTGTAATAGCATTTGGCTTACATATGCCAAGAA 1227
 QY 293 ValArgAlaLysArgSerSerLysMetTyrLeuLysThrArgSerGlnMetProTyrLys 312
 DB 1228 ATGAGGAACAAGAGGAAACAGCAAAATGTACCTTAAACCCCGGCGGCGATGCCCTTCAGA 1287
 QY 313 ValPheHisTyrGlnValLysIleHisPheSerGlyThrGluSerGluThrHisThrAsn 332
 DB 1288 GTTTACCATTCAGATGAATAATCCATGCTTTCAGTTTACAGAAACATGGGAGAAATGAG 1347
 QY 333 GlnAlaPheGluIleSerLeuTyrGlyThrValAlaGluSerGluAsnIleProPheThr 352
 DB 1348 CCCACCTTTTACCTCACCTTTTATGCACTTAATGCAATTCAGACTCTGCCACTCGAA 1407
 QY 353 LeuProGlu---ValSerThrAsnLysThrTyrSerPheLeuIleTyrThrGluValAsp 371
 DB 1408 ATAGTGGAGCGGATCGAGCAGATGCCCAACACTTCTGTGTCTACACGAGGAGGAC 1467
 QY 372 IleGlyGluLeuMetLeuLysLeuLysTrpLysSerAspSerTyrPheSerTrpSer 391
 DB 1468 TTGGAGACCTCTTGAAGATCCAGCTACCTGGGAGGGGGCTCTCAG---TCTTGTGATC 1524
 QY 392 AspTrpTrpSer-----SerProGly-----Phe 399
 DB 1525 AACCTGTGAAGAGATTTCGAGCTACCTGTCTCAACCCCGCAACCCGCGGAGGAGCTG 1584
 QY 400 AlaIleGlnLysIleArgValLysAlaGlyGluThrGlnLysLysValIlePheCysSer 419
 DB 1585 AATATCAGGCGCATCGGGTGAAGTCTGGGAAACCCAGCGGAACCTGACATTTTGTACA 1644

QY 420 ArgGluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHis 439
 Db 1645 GAAGACCTCAGAACACCATATATCCAGCGGGAGCTCTGGTTTCGAAGTCTCGG 1704
 QY 440 Asp 440
 Db 1705 GAT 1707

RESULT 11

US-10-211-462-228
 ; Sequence 228, Application US/10211462
 ; Publication No. US20040033495A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Murray, Richard
 ; APPLICANT: Glynn, Richard
 ; APPLICANT: Watson, Susan R.
 ; APPLICANT: Aziz, Natasha
 ; APPLICANT: Eos Biotechnology, Inc.
 ; TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and
 ; FILE OF INVENTION: Methods of Screening for Angiogenesis Modulators
 ; FILE REFERENCE: 018501-006200US
 ; CURRENT APPLICATION NUMBER: US/10/211,462
 ; PRIOR FILING DATE: 2003-02-13
 ; PRIOR APPLICATION NUMBER: US 09/784,356
 ; PRIOR FILING DATE: 2001-02-14
 ; PRIOR APPLICATION NUMBER: US 09/791,390
 ; PRIOR FILING DATE: 2001-02-22
 ; PRIOR APPLICATION NUMBER: US 60/310,025
 ; PRIOR FILING DATE: 2001-08-03
 ; PRIOR APPLICATION NUMBER: US 60/334,244
 ; PRIOR FILING DATE: 2001-11-29
 ; NUMBER OF SEQ ID NOS: 230
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 228
 ; LENGTH: 3927
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-211-462-228

Alignment Scores:
 Pred. No.: 6,42e-129 Length: 3927
 Score: 1161.00 Matches: 216
 Percent Similarity: 69.16% Conservative: 89
 Best Local Similarity: 48.98% Mismatches: 118
 Query Match: 18 Indels: 6
 DB: 16 Gaps: 6

US-10-019-341-3 (1-448) x US-10-211-462-228 (1-3927)

QY 13 LysPheAlaLeuArgThrProGluAspThrAlaGluAspThrCysHisLeuLeuProGly 32
 Db 400 AGTTTAACTCCGACCTCCAGGACCCAGAGCATGAAGATGCTCCTCCGTCGGC 459
 QY 33 ValAlaGluSerValAlaThrCysHisSerHisSerSerLysThrPheMetValLe 52
 Db 460 CACAGCCAGCCCTTAGAGACTGAGTTCACATGACAGTAAACCTTTTCATCATT 519
 QY 53 HisGlyTrpThrValThrGlyMetLysGluSerTrpValProLysLeuValAlaLeu 72
 Db 520 CACGGATGAGCATGAGCGGTATCTTTGAAACCTGGCTGCACAACTCGTGCAGCCCTG 579
 QY 73 TyrLysArgGluProAspSerAsnValLeValValAspThrLeuSerArgAlaGlnGlu 92
 Db 580 CACACAGAGAAAGACGCCAATGTAGTTGTGCTGCTCCCTCCCTCCCTCCCTCCAG 639
 QY 93 HisTyrProValSerAlaGlyTyrThrLysLeuValGlnAspValAlaAatgPheLe 112
 Db 640 CTTTACAGGATCGGTCAATATACAGGGTGTGGACACAGCATTCGACGATGCTC 699
 QY 113 AsnTrpMetGluGluPheAsnTyrProLeuAspAsnValHisLeuLeuGlyTyrSer 132
 Db 700 GACTGGCTGAGGAGAGGACGATTTTCTCTCGGGAATGTCACCTTGATCGGCTACAGC 759

QY 133 LeuGlyAlaHisAlaAlaGlyLeuAlaGlySerLeuThrAsnLysLysValAsnArgLe 152
 Db 760 CTCGGAGCGCACGTGCGGGTATGAGGCACTTCGTGAAAGAACGCTGGCCGGAATC 819
 QY 153 ThrGlyLeuAspProAlaGlyProAsnPheGluTyrAlaGluAlaProSerArgLeuSer 172
 Db 820 ACAGGTTTGGATCTCTCGCGGGCCCATGTTTGAAGGGCGGCACATCCACAGAGGCTCTCT 879
 QY 173 ProAspAlaAspPheValLeuHisThrPheThrArgGlySerProGlyArg 192
 Db 880 CCGGACGATGACAGATTTGTGATGTCCTCCACACCTACACCGCT---TCTTCGGCTTG 936
 QY 193 SerIleGlyIleGlnLysProValGlyHisValAspIleTyrProAsnGlyGlyThrPhe 212
 Db 937 AGCATTTGTTTATTCAGATGCTTGGGCGCACATTCATCTACCCCAATGGGGTGAATTC 996
 QY 213 GlnProGlyCysAsnIleGlyGluAlaIleArgValIleAlaGluArgGlyLeuGlyAsp 232
 Db 997 CAGCCAGGCTGTGGACTCAACGATGCTTTGGGATCAATTTGCA-----TATGGAACA 1047
 QY 233 ValAspGlnLeuValLysCysSerHisGluArgSerIleHisLeuPheIleAspSerLeu 252
 Db 1048 ATCAGAGGCTGTAAATGTGAGCATGAGCGCGCTCCACCTCTTTTGTGACTCTCTG 1107
 QY 253 LeuAsnGluGluAsnProSerLysAlaTyrArgCysSerSerLysGluAlaPheGluLys 272
 Db 1108 GTGAATCAGGACAGCCGAGTTTTCCTTCAGTGCATGCTCCCAATCGCTTCARAAG 1167
 QY 273 GlyLeuCysLeuSerCysArgLysAsnArgCysAsnAsnLeuGlyTyrGluLeuAsnLys 292
 Db 1168 GGGATCTCTGAGCTGCGCAAGACCGTTGTAATAGCATTTGGCTCAACATGCCAAGAAA 1227
 QY 293 ValArgAlaLysArgSerSerLysMetTyrLeuLysThrArgSerGlnMetProTyrLys 312
 Db 1228 ATGAGAACAGAGAGACAGCAAAATGTACCTAAACCCCGGAGGATGCTCTTCAGA 1287
 QY 313 ValPheHisTyrGlnValLysIleHisPheSerGlyThrGluSerGluThrHisThrAsn 332
 Db 1288 GTTTACCATTCAGATGAAATCCATGCTCTTCAGTTACAGACATCGGAGAAATTGAG 1347
 QY 333 GlnAlaPheGluLeuSerLeuTyrGlyThrValAlaGluSerGluAsnIleProPheThr 352
 Db 1348 CCCACCTTTTACGTACCCCTTTATGGCACTAATGCAGATTCAGACCTCTCCACTGGAA 1407
 QY 353 LeuProGlu---ValSerThrAsnLysThrTyrSerPheLeuIleTyrThrGluValAsp 371
 Db 1408 ATAGTGAGCGGATCGAGAGATGCCAACACCTTCCTGGTCTACACGAGGAGGAC 1467
 QY 372 IleGlyGluLeuLeuMetLeuLysLeuLysTrpLysSerAspSerTyrPheSerTrpSer 391
 Db 1468 TTGGAGACCTCTTTGAAGATCCAGCTCACCTGGAGGGGGCTCTCAG---TCTTGGTAC 1524
 QY 392 AspTrpTrpSer-----SerProGly-----Phe 399
 Db 1525 AACCTGTGAGGAGGAGTTTCGAGCTACCTGTCTCAACCCCGCAACCCCGAGGAGCTG 1584
 QY 400 AlaIleGlnLysIleArgValLysAlaGlyGluThrGlnLysLysValIlePheCysSer 419
 Db 1585 AATATCAGGCGATCCCGGTGAAGCTCTGGGGAACCCAGCGGAACTGACATTTTGTACA 1644
 QY 420 ArgGluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHis 439
 Db 1645 GAAGACCTGAGAACACCATATCCCGAGCGGGAGCTCTGGTTTCCCAAGTGTGG 1704
 QY 440 Asp 440
 Db 1705 GAT 1707

RESULT 12

US-10-342-887-1234
 ; Sequence 1234, Application US/10342887
 ; Publication No. US20040058340A1

Db 937 AGCATTGGTATTTCAGATGCTGTGGGCACATGTGACATCTACCCCAATGGGGTGACTTC 996
Qy 213 GlnProGlyCysAsnIleGlyGluAlaIleArgValIleAlaGluArgGlyLeuGlyAsp 232
Db 997 CAGCCAGGCTGTGGACTCAACGATGCTTGGGATCAATTGCA-----TATGGAACA 1047
Qy 233 ValAspGlnLeuValLysCysSerHisGluArgSerIleHisLeuPheIleAspSerLeu 252
Db 1048 ATCACAGAGTGTGTAATAATGTGAGCATGAGCGAGCGCTGCACCTCTTTGTTGACTCTCTG 1107
Qy 253 LeuAspGlnGluAsnProSerLysAlaTyrArgCysSerSerLysGluAlaPheGluLys 272
Db 1108 GTCAATCAGACAAGCCGAGTTTGTGCTTCCAGTGCACATCTCCAAATCGCTTCAAAAG 1167
Qy 273 GlyLeuCysLeuSerCysArgLysAsnArgCysAsnAsnLeuGlyTyrGluIleAsnLys 292
Db 1168 GGGATCTGTCTGAGCTGCCGCAAGAACCTGTTATAGCATTTGGCTACAAATGCCAAGAAA 1227
Qy 293 ValArgAlaLysArgSerLysMetTyrLeuLysThrArgSerGlnMetProTyrLys 312
Db 1228 ATGAGGAACAAGAGGAACAAGCAAAATGTACTAAAAACCCGGCGCAGCATGCTTTTCAGA 1287
Qy 313 ValPheHisTyrGlnValLysIleHisPheSerGlyThrGluSerGluThrHisThrAsn 332
Db 1288 GTTTACCATTTATCAGATGAAATCCCATGTCTTCAGTTACAAGAACAATGGGAGAAATTGAG 1347
Qy 333 GlnAlaPheGluIleSerLeuTyrGlyThrValAlaGluSerGluAsnIleProPheThr 352
Db 1348 CCCACCTTTTACGTACCCCTTTATGGCATTAATGCAGATTCACAGACTCTGCCACTGGAA 1407
Qy 353 LeuProGlu---ValSerThrAsnLysThrTyrSerPheLeuIleTyrThrGluValAsp 371
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Db 1525 AACCTGTGAAGAGGATTTCCGAGTACTCTCTCAACCCGCAACCCGCGAGCGGAGCTG 1584
Qy 400 AlaIleGlnLysIleArgValLysAlaGlyGluThrGlnLysLysValIlePheCysSer 419
Db 1585 AATATCAGCGCATCCGGGTGAAGTCTGGGGAAACCCAGCGGAAACTGACATTTTGTACA 1644
Qy 420 ArgGluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHis 439
Db 1645 GAAGACCTGTGAACAACACCATATCCCGAGCGCGGAGCTCTGGTTTCGAAGTGTCTGG 1704
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Db 1705 GAT 1707
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US-10-319-915-4
; Sequence 4, Application US/10311915
; Publication NO. US20040115653A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF ENDOTHELIAL LIPASE EXPRESSION
; FILE REFERENCE: RTS-0447
; CURRENT APPLICATION NUMBER: US/10/319,915
; CURRENT FILING DATE: 2002-12-12
; NUMBER OF SEQ ID NOS: 279
; SEQ ID NO 4
; LENGTH: 3927
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; FEATURE:
; NAME/KEY: CDS

LOCATION: (253) ... (1755)
US-10-319-915-4

Alignment Scores:
Pred. No.: 6,42e-129 Length: 3927
Score: 1161.00 Matches: 216
Percent Similarity: 69.16% Conservatives: 89
Best Local Similarity: 48.98% Mismatches: 118
Query Match: 48.68% Indels: 18
DB: 17 Gaps: 6

US-10-019-341-3 (1-448) x US-10-319-915-4 (1-3927)

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QY 13 LysPheAlaLeuArgThrProGluAspThrAlaGluAspThrCysHisLeuLeuProGly 32
Db 400 AGGTTTAACTCCGACCTCCAGGACCCAGAGCATGTAAGGATGTACCTCTCCGTCGGC 459

QY 33 ValAlaGluSerValAlaThrCysHisPheAsnHisSerSerLysThrPheMetValile 52
Db 460 CACAGCCAGCCCTTAGAGACTGCAGTTTCAACATGACAGCTAAACCTTTTTCATCAT 519

QY 53 HisGlyTrpThrValThrGlyMetTyGluSerTrpValProLysLeuValAlaLeu 72
Db 520 CACGATGACATGACGCGGTATCTTGAATACTGGCTGCACAAACTCGTGTACGCGCTG 579

QY 73 TyrLysArgGluProAspSerAsnValileValValAspTrpLeuSerArgAlaGlnGlu 92
Db 580 CACACAGAGAGAGAGAGCCCATGTAGTTGGTTGACTGGCTCCCCCTGGCCACCCAG 639

QY 93 HisTyrProValSerAlaGlyTyrThrLysLeuValGlyGlnAspValAlaArgPheile 112
Db 640 CTTTACCGGATCGGTCAATAATACAGGGTGGTGGACACAGCATTCGCCAGGATGTC 699

QY 113 AsnTrpMetGluGluGluPheAsnTyrProLeuAspAsnValHisLeuLeuGlyTyrSer 132
Db 700 GACTGGCTGCGAGGAGAGAGCATTTTCTCTCGGGAATGTCCACTTCATCGGCTACAGC 759

QY 133 LeuGlyAlaHisAlaAlaGlyIleAlaGlySerLeuThrAsnLysLysValAsnArgile 152
Db 760 CTCGAGCGCAGCTGGCGGGTATGCAGCAACTCTGTGAAGAACCGTGGCGGCAATC 819

QY 153 ThrGlyLeuAspProAlaGlyProAsnPheGluTyrAlaGluAlaProSerArgLeuSer 172
Db 820 ACAGTTTGGATCTCGCGGGCCCATGTTTGAAGGGCGGACATCCACAGAGGCTCTCT 879

QY 173 ProAspAlaAspPheValAspValLeuHisThrPheThrArgGlySerProGlyArg 192
Db 880 CCGACGATGACGATTTGTGGATGTCCTCACACCTACACGCGT---TCCTCGGCTTG 936

QY 193 SerileGlyIleGlnLysProValGlyHisValAspIleTyrProAsnGlyGlyThrPhe 212
Db 937 AGCATTTGATTCAGATGCTGTGGGCACATTCACATCTACCCCAATGGGGGTGACTTC 996

QY 213 GlnProGlyCysAsnIleGlyGluAlaIleArgValileAlaGluArgGlyLeuGlyAsp 232
Db 997 CAGCAGGCTGTGACTCAACGATGCTCTGGATCAATTGCA-----TATGGACA 1047

QY 233 ValAspGlnLeuValLysCysSerHisGluArgSerIleHisLeuPheIleAspSerLeu 252
Db 1048 ATCACAGGTTGGTAAATATGACATGAGCAGCGCGCTCCACCTCTTTTGTGACTCTCTG 1107

QY 253 LeuAsnGluGluAsnProSerLysAlaTyrArgCysSerSerLysGluAlaPheGluLys 272
Db 1108 GTGAATCAGGACAGCCGAGTTTGGCTTCAGTGTGACTGACTCAATTCGCTTCAAAAG 1167

QY 273 GlyLeuCysLeuSerCysArgLysAsnArgCysAsnAsnLeuGlyTyrGluIleAsnLys 292
Db 1168 GGGATGTCTGAGCTGCCGCAAGACCGTTGTAATAGCATTTGGCTACATGCAAGAAA 1227

QY 293 ValArgAlaLysArgSerSerLysMetTyriLeuLysThrArgSerGlnMetProTyLys 312
Db 1228 ATGAGGAACAGAGGAAACAGAAAATGTACTTAAACCCCGGCGAGCATGCTTTTCAGA 1287

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QY 313 ValPheHisTyrGlnValLysIleHisPheSerGlyThrGluSerGluThrHisThrAsn 332
Db 1288 GTTACCATTATCAGATGAAATCCATGCTTTCAGTTTACAAGAACATGGGAGAAATTGAG 1347

QY 333 GlnAlaPheGluIleSerLeuTyrGlyThrValAlaGluSerGluAsnIleProPheThr 352
Db 1348 CCCACCTTTTACGTACCTCCCTTTATGCACATAATGCAGATTCACCACTCTGCCACTGGAA 1407

QY 353 LeuProGlu---ValSerThrAsnLysThrTyrSerPheLeuIleTyrThrGluValAsp 371
Db 1408 ATAGTGGAGCGGATCGAGCAGATGCCAACACCTTCTGTCTTACACCGAGGAGGAC 1467

QY 372 IleGlyGluLeuMetLeuLysLeuTyrLysSerAspSerTyrPheSerTrpSer 391
Db 1468 TTGGAGAGACTCTTGAAGATCAGCTCACCTGGAGGGGGCTCTCAG---TCTTGGTAC 1524

QY 392 AspTrpTrpSer-----SerProGly-----Phe 399
Db 1525 AACCTGTGGAAGAGATTTCGACGTACCTGTCTCAACCCCGCAACCCCGGAGGAGCTG 1584

QY 400 AlaIleGlnLysIleArgValLysAlaGlyGluThrGlnLysValIlePheCysSer 419
Db 1585 AATATCAGCGCATCGGGTGAAGTCTGGGNAACCCAGCGGAACTGACATTTGTATCA 1644

QY 420 ArgGluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHis 439
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QY 440 Asp 440
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RESULT 14
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; Publication No. US20030166903A1
; GENERAL INFORMATION:
; APPLICANT: Astromoff, Anna
; APPLICANT: Bandman, Olga
; APPLICANT: Cocks, Benjamin G.
; TITLE OF INVENTION: GENES ASSOCIATED WITH VASCULAR DISEASE
; FILE REFERENCE: PA-0049 US
; CURRENT APPLICATION NUMBER: US/10/133,013
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/287,067
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 271
; SOFTWARE: PERL Program
; SEQ ID NO 213
; LENGTH: 4315
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030166903A1 400203.1
US-10-133-013-213

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US-10-019-341-3 (1-448) x US-10-133-013-213 (1-4315)

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QY 33 ValAlaGluSerValAlaThrCysHisPheAsnHisSerSerLysThrPheMetValile 52
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Qy 73 TyrLysArgGluProAspSerAsnValleValValAspTrpLeuSerArgAlaGlnGlu 92
Db 745 CACACAGAGAGAAAGACGCAATGTAGTTGTGGTTGACTGGCTCCCTCGGCCACACAG 804
Qy 93 HisTyrProValSerAlaGlyTyrThrLysLeuValGlyGlnAspValAlaArgPheIle 112
Db 805 CTTTACACGGATGCGGTCAATTAATACAGGGTGGTGGACACAGCATTCAGGATGCTC 864
Qy 113 AsnTrpMetGluGluGluPheAsnTyrProLeuAspAsnValHisLeuLeuGlyTyrSer 132
Db 865 GACTGCTGCAGGAGAGGACGATTTTCTCTCGGGAATGCTCACTGATCGCTTACAGC 924
Qy 133 LeuGlyAlaHisAlaAlaGlyIleAlaGlySerLeuThrAsnLysLysValAsnArgIle 152
Db 925 CTCGAGCGGCAGCTGGCGGGTATGACGACACTTCGTCAAGAGAACCGTGGCGCAATC 984
Qy 153 ThrGlyLeuAspProAlaGlyProAsnPheGluTyrAlaGluAlaProSerArgLeuSer 172
Db 985 ACAGTTTGGATTCCTGCGGGCCCATGTTTGAAGCGGCGACATCCACAGAGGCTCT 1044
Qy 173 ProAspAlaAspPheValAspValLeuHisThrPheThrArgGlySerProGlyArg 192
Db 1045 CCGGACGATGCAGATTTTGTGATGCTCTCCACACTACACGCT---TCTTTCGGCTTG 1101
Qy 193 SerIleGlyIleGlnLysProValGlyHisValAspIleTyrProAsnGlyGlyThrPhe 212
Db 1102 AGCATTTGGTATTTCAGATGCTGTGGCCCATGTGATCATCTACCCCAATGGGGTGACTTC 1161
Qy 213 GlnProGlyCysAsnIleGlyGluAlaIleArgValIleAlaGluArgGlyLeuGlyAsp 232
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Qy 233 ValAspGlnLeuValLysCysSerHisGluArgSerIleHisLeuPheIleAspSerLeu 252
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Qy 253 LeuAsnGluGluAsnProSerLysAlaTyrArgCysSerSerLysGluAlaPheGluLys 272
Db 1273 GTGAATCAGCAAGACCGAGTTTGGCTTCCAGTGCACGACTCCCAATCGCTTCAAAAG 1332
Qy 273 GlyLeuCysLeuSerCysArgLysAsnArgCysAsnAsnLeuGlyTyrGluIleAsnLys 292
Db 1333 GGGATCTGTGAGCTGCCGCAAGAACCGTTGTAATAGCATTTGGCTACATGCGTTCAGAA 1392
Qy 293 ValArgAlaLysArgSerLysMetTyrLeuLysThrArgSerGlnMetProTyrLys 312
Db 1393 ATGAGGAACAAGAGGAACAGCAAAATGTACTTAAACACCGGCGGACATCGCTTTTCA 1452
Qy 313 ValPheHisTyrGlnValLysIleHisPheSerGlyThrGluSerGluThrHisThrAsn 332
Db 1453 GTTTACCATTTATCAGATGAAATCCCATGCTTCAGTTACAGAACATGGGAGAAATTGAG 1512
Qy 333 GlnAlaPheGluIleSerLeuTyrGlyThrValAlaGluSerGluAsnIleProPheThr 352
Db 1513 CCACACTTTACGTCACCTTTATGGCACTAATGCAATTCACGACTCTGCCACTGGAA 1572
Qy 353 LeuProGlu---ValSerThrAsnLysThrTyrSerPheLeuIleTyrThrGluValAsp 371
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Qy 372 IleGlyGluLeuLeuMetLeuLysLeuLysTrpLysSerAspSerTyrPheSerTrpSer 391
Db 1633 TTGGGAGACCTCTTTGAAGATCCAGCTCACCTGGGAGGGGGCTCTCAG---TCTTGTATC 1689
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Db 1690 AACCTGTGGAGGAGTTTCGACGACTGCTGTCTCAACCCCGCAACCCCGGAGCGGAGCTG 1749

Qy 400 AlaIleGlnLysIleArgValLysAlaGlyGluThrGlnLysLysValIlePheCysSer 419
Db 1750 AATATCAGGCGCATCCGGTGAAGTCTGGGGAAACCCAGCGAACTGACATTTTGTACA 1809
Qy 420 ArgGluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHis 439
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; Publication No. US20040115653A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: MODULATION OF ENDOTHELIAL LIPASE EXPRESSION
; FILE REFERENCE: RTS-0447
; CURRENT APPLICATION NUMBER: US/10/319,915
; CURRENT FILING DATE: 2002-12-12
; NUMBER OF SEQ ID NOS: 279
; SEQ ID NO 99
; LENGTH: 2227
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (275) ... (1777)
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Qy 54 GlyTrpThrValThrGlyMetTyrGluSerTrpValProLysLeuValAlaLeuTyr 73
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Qy 74 LysArgGluProAspSerAsnValIleValValAspTrpLeuSerArgAlaGlnGluHis 93
Db 605 ATCAGAGAGAAAGATGCTAACGTCGTGGTGGTTGACTGGCTGCCCTGCCTCATCGCTG 664
Qy 94 TyrProValSerAlaGlyTyrThrLysLeuValGlyGlnAspValAlaArgPheIleAsn 113
Db 665 TACACGGATGCTCAATAACACCGAGGTGGTGGGACAGAGATAGTGGGATGCTTGAC 724
Qy 114 TrpMetGluGluGluPheAsnTyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeu 133
Db 725 TGGCTGACAGAGAGAGAGAGAGTCTCTCTTGGGAACTTTCATTTGATGCTACAGCCTT 784
Qy 134 GlyAlaHisAlaAlaGlyIleAlaGlySerLeuThrAsnLysLysValAsnArgIleThr 153
Db 785 GGAGCACACGCTGGCTGGATACGCTGGCACTTTGTGAAAGGAAACAGTGGGAGGATCCT 844
Qy 154 GlyLeuAspProAlaGlyProAsnPheGluTyrAlaGluAlaProSerArgLeuSerPro 173

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Db      905 GAGCATGCGAGACTTGTGGATGTCCTGCGCATACCTACACGCTG---TCCTTTGGCTTGAGC 961
QY      194 IleGlyIleGlnLysProValGlyHisValAspIleTyrProAsnGlyGlyThrPheGln 213
Db      962 ATTGGGATTCGATCGCTGTGGGTACATTCATGACATCTATCCCAATGGCGGTGACTTCCAG 1021
QY      214 ProGlyCysAsnIleGlyGluAlaIleArgValIleAlaGluArgGlyLeuGlyAspVal 233
Db      1022 CCAGGCTGGGATTCATGAT-----GTCACTGGATCTTTGCATATGGAACAATC 1072
QY      234 AspGlnLeuValLysCysSerHisGluArgSerIleHisLeuPheIleAspSerLeuLeu 253
Db      1073 TCAGAGATGGTGAATGCGAGCGAGCGCGGTACACCTCTTTGTGCACTCTCTGTGTG 1132
QY      254 AsnGluGluAsnProSerLysAlaTyrArgCysSerSerLysGluAlaPheGluLysGly 273
Db      1133 AATCAGGACAAGCCAGCTTTGCCCTTCCAGTGCACAGACTCCAGCGCTTCAAAAGGGA 1192
QY      274 LeuCysLeuSerCysArgLysAsnArgCysAsnAsnLeuGlyTyrGluIleAsnLysVal 293
Db      1193 ATCTGCCCTCAGCTGCCGAAGAACCGTTGTATAACATTGGCTACACGCCCAAGAAATG 1252
QY      294 ArgAlaLysArgSerLysMetTyrLeuLysThrArgSerGlnMetProTyrLysVal 313
Db      1253 AGAAGAGAGAGATAGCAAAATGTATTTAAACCCGGCTGGCATGCCCTTTCAAAGTT 1312
QY      314 PheHisTyrGlnValLysIleHisPheSerGlyThrGluSerGluThrHisThrAsnGln 333
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QY      354 ProGlu---ValSerThrAsnLysThrTyrSerPheLeuIleTyrThrGluValAspIle 372
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QY      393 TrpTrp-----SerSerProGly-----PheAla 400
Db      1550 CTGTGGAATGAGTTTCGCAACTACCTGTCTCAACCCAGCAACCCCTCGAGGAGCTGTAC 1609
QY      401 IleGlnLysIleArgValLysAlaGlyGluThrGlnLysLysValIlePheCysSerArg 420
Db      1610 ATCGGCGAATTGGTGTCAATCTGGGGAACCCAGCGCAAGAGTACATTTGCACCTCAA 1669
QY      421 GluLysVal---SerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHis 439
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Job time : 716 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: October 24, 2004, 17:57:24 ; Search time 4360 Seconds
(without alignments)

3744.266 Million cell updates/sec

Title: US-10-019-341-3

Perfect score: 2385

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Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
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-NO.WMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*

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2: gb_est2: *
3: gb_hc: *
4: gb_est3: *
5: gb_est4: *
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7: gb_est6: *
8: gb_gsl1: *
9: gb_gsl2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2236.5	93.8	1424	9 AY410291	AY410291 Mus muscu
3	2233.5	93.6	1950	3 AK086023	AK086023 Mus muscu
4	2233.5	93.6	2018	3 AK045064	AK045064 Mus muscu
5	2233.5	93.6	2054	3 AK003645	AK003645 Mus muscu
6	2229.5	93.5	2018	3 AK079446	AK079446 Mus muscu
7	2218.5	93.0	1899	3 AK017272	AK017272 Mus muscu
8	1834	76.9	1427	9 AY410290	AY410290 Pan trogl
9	1553	65.1	2791	3 CR605471	CR605471 full-leng

10	1534	64.3	1063	1	AL539198	AL539198
11	1463	61.3	1076	5	BX418566	BX418566
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13	1280	53.7	812	7	CO734715	CO734715
14	1274.5	53.4	896	4	BI599196	BI599196
15	1259.5	52.8	800	7	CO587716	CO587716
16	1259	52.8	758	7	CK359169	CK359169
17	1253	52.5	776	7	CK479340	CK479340
18	1248	52.3	735	7	CK359202	CK359202
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21	1205	50.5	965	5	BQ926353	BQ926353
22	1190	49.9	942	7	CF408927	CF408927
23	1171	49.1	938	5	BX441464	BX441464
24	1147	48.1	768	2	BE911230	BE911230
25	1138.5	47.7	772	4	BG429264	BG429264
26	1130	47.4	657	6	CB442273	CB442273
27	1107	46.4	645	5	BQ695136	BQ695136
28	1105	46.3	744	6	CD104574	CD104574
29	1088.5	45.6	844	5	BU470625	BU470625
30	1087	45.6	892	7	CF551941	CF551941
31	1086	45.5	804	1	AU130815	AU130815
32	1085	45.5	825	7	CK313328	CK313328
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ALIGNMENTS

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VERSION	AY410289.1	GI:39766257				
KEYWORDS	GSS.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarimal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.					
TITLE	1 (bases 1 to 1427)					
JOURNAL	Science 302 (5652), 1960-1963 (2003)					
PUBMED	14671302					
REFERENCE	2 (bases 1 to 1427)					
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarimal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.					
TITLE	Direct Submission					
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA					
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.					
FEATURES	Location/Qualifiers					
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ORIGIN

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 Score: 2385.00
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-10-019-341-3 (1-448) x AY410289 (1-1427)

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 QY 21 AspThrAlaGluAspThrCysHisLeuIleProGlyValAlaGluSerValAlaThrCys 40
 Db 142 GACACAGCTGAGGACATTCGCCACCTCATTCGCCGAGTAGCAGATTCGGTGGCTACCTGT 201
 QY 41 HisPheAsnHisSerSerLysThrPheMetValIleHisGlyThrThrValThrGlyMet 60
 Db 202 CATTTCAATCAGCAGCAAAACCTTCATGGTGATCCATGGCTGGACGGTAAACGGAATG 261
 QY 61 TyrGluSerTrpValProLysLeuValAlaAlaLeuTyrLysArgGluProAspSerAsn 80
 Db 262 TATGAGAGTTGGTGGCAAAACTTGTGGCGGCCCTGTACAAGAGAGAACACGACTCCAAAT 321
 QY 81 ValIleValValAspTrpLeuSerArgAlaGlnGluHisTyrProValSerAlaGlyTyr 100
 Db 322 GTCATTTGGTGGAGCTGGCTGTACGGCTCAGGAGCATTTACCATGTGCCGGGGCTAC 381
 QY 101 ThrLysLeuValGlyGlnAspValAlaArgPheIleAsnTrpMetGluGluGluPheAsn 120
 Db 382 ACCAACTGTGGACAGATGTGGCCCGCTTTATCACTGGATGGAGGAGAGTTAAAC 441
 QY 121 TyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeuGlyValAlaHisAlaGlyIle 140
 Db 442 TACCTCTGGACAAATTCATCTCTTGGGATACAGCTTGGAGCCCATGCTGCTGGCAT 501
 QY 141 AlaGlySerLeuThrAsnLysLysValAsnArgIleThrGlyLeuAspProAlaGlyPro 160
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 QY 161 AsnPheGluTyrAlaGluAlaProSerArgLeuSerProAspAspAlaAspPheValAsp 180
 Db 562 AACTTTGAGTATGACAGAGCCCGAGTGGCTTCTTCTCTGATGATGATGATGATGATGAT 621
 QY 181 ValLeuHisThrPheThrArgGlySerProGlyArgSerIleGlyIleGlnLysProVal 200
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 QY 201 GlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGlu 220
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 QY 261 AlaTyrArgCysSerSerLysGluAlaPheGluLysGlyLeuCysLeuSerCysArgLys 280
 Db 862 GCCTACAGGTGCAATTCAGAGGAGCCCTTTGAGAAAGGGCTCTGCTTGTAGTGTAGAAAG 921

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 QY 301 MetTyrLeuLysThrArgSerGlnMetProTyrLysValPheHisTyrGlnValLysIle 320
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 QY 321 HisPheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGluIleSerLeuTyr 340
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 DEFINITION genomic survey sequence.
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 VERSION AY410291.1
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 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 1424)
 AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PubMed 14671302
 REFERENCE 2 (bases 1 to 1424)
 AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering
 them based on alignment.
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Query Match:     93.77%        Indels:      1
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US-10-019-341-3 (1-448) x AY410291 (1-1424)

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PUBMED REFERENCE AUTHORS	11076861 4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)	Percent Similarity: 95.98% Best Local Similarity: 93.53% Query Match: 93.65% DB: 3 US-10-019-341-3 (1-448) x AK086023 (1-1950)	Conservative: 11 Mismatches: 17 Indels: 1 Gaps: 1
TITLE JOURNAL AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)	QY 1 AlaAspGlnArgArgAspPheIleAspIleGluSerLysPheAlaLeuArgThrProGlu 20 Db 101 GCACACGGGGAAGAGATTTCTCAGACATCGAAGCAAAATTTGCCCTAAGAGCCCTGAA 160 QY 21 AspThrAlaGluAspThrCysHisLeuIleProGlyValAlaGluSerValalaThrCys 40 Db 161 GACACAGCTGAGGACACTTGTCACTCATCTCGATTAGCAGACTCTGTGTCAACTGC 220	
TITLE JOURNAL AUTHORS	6 (bases 1 to 1950) Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, P., Imotani, K., Iehii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, K., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)	QY 41 HisPheAsnHisSerSerLysThrPheMetValIleHisGlyThrValThrGlyMet 60 Db 221 CACTTCAACACAGCAGCAGACCTTCGTGTGTATCCATGATGACGCGGTACCGGAATG 280 QY 61 TyrGluSerTrpValProLysLeuValAlaAlaLeuTyrLysArgGluProAspSerAsn 80 Db 281 TATGAGAGTTGGTGCCCAACTTGTGGCCGCCCTGTACAGAGAGAACTGACTCCAAAT 340 QY 81 ValIleValValAspTrpLeuSerArgAlaGlnGluHisTyrProValSerAlaGlyTyr 100 Db 341 GTCATTGTAGTACTGTTGTATGTCGGCCAGCAACATTATCCAGTGTCACTGGCTAC 400	
TITLE JOURNAL	Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/ URL: http://fantom.qualifiers	QY 101 ThrLysLeuValGlyGlnAspValAlaArgPheIleAsnTrpMetGluGluPheAsn 120 Db 401 ACCAAGCTGGTGGGAAATGATGTGGCCAGATTTCATCACTGGATGGAGAGAGTTTAA 460 QY 121 TyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeuGlyValAlaHisAlaGlyIle 140 Db 461 TACCCCTTAGACACAGTCCACTCTTAGGTACACCTTGGAGCCCATGCTCTGGCGTA 520	
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 VERSION AK045064.1 GI:26337040
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 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
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 1
 Carninci, P. and Hayashizaki, Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636
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 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 20499374
 PUBMED 11042159
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 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Inoue, K., Takaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Matsuo, H., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE 20530913
 PUBMED 11076861
 4
 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409, 685-690 (2001)
 MEDLINE 11076861
 PUBMED 11076861
 5
 The FANTOM Consortium and the RIKEN Genome Exploration Research

Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 6 (bases 1 to 2018)

AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hasegawa, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (16-JUL-2001) Yoshinori Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216]

COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Tissues were provided by Dr. Tomohiro Kono (Department of Animal Science, Tokyo University of Agriculture, 1737 Hunko Aisugi City, Kanagawa Prefecture, Japan) whose assistance we gratefully acknowledge.

Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/

URL: http://fantom.gsc.riken.jp/

FEATURES
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1. 2018
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ORIGIN

Alignment Scores:
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 Percent Similarity: 95.98% Conservative: 11
 Best Local Similarity: 93.53% Mismatches: 17
 Query Match: 93.65% Indels: 1
 DB: 3 Gaps: 1

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US-10-019-341-3 (1-448) x AK045064 (1-2018)

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Qy 441 LysSerLeuAsnLysLysSerGly 448
Db 1489 AAGTCTCTG---AAGAAGTCTGGC 1509

RESULT 5
AK002645 2054 bp mRNA linear HTC 03-APR-2004
LOCUS Mus musculus adult male kidney cDNA, RIKEN full-length enriched
DEFINITION library, clone:061001C21 product:lipoprotein lipase, full insert
sequence.
ACCESSION AK002645
VERSION AK002645.1 GI:12832782
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 Carninci, P. and Hayashizaki, Y.
AUTHORS High-efficiency full-length cDNA cloning
TITLE Meth. Enzymol. 303, 19-44 (1999)
JOURNAL 99279253
MEDLINE PUBMED 10349636
REFERENCE 2
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE PUBMED 20499374
REFERENCE 3
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
```

REFERENCE
AUTHORS

6 (bases 1 to 2054)
 Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H.,
 Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y.,
 Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K.,
 Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M.,
 Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M.,
 Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K.,
 Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C.,
 Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Saeki, D.,
 Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y.,
 Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T.,
 Tejima, Y., Toyota, T., Yamamura, T., Yasunishi, A., Yoshida, K.,
 Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
 Direct Submission
 Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,
 URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222,
 Fax: 81-45-503-9216)
 Please visit our web site (<http://genome.gsc.riken.jp/>) for further
 details.

COMMENT

cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN,
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues. First strand cDNA was primed with a primer
 [5', GAGAGAGAGCGCGCCACTCGATCTTTTCTTTTNN 3'], cDNA was
 prepared by using triazole thermo-activated reverse transcriptase
 and subsequently enriched for full-length by cap-trapper. cDNA went
 through one round of normalization to Rot = 5.0. Second strand cDNA
 was prepared with the primer adapter of sequence [5',
 GAGAGAGAGAGATCCAGAGCTCAATATTTAATTAACCCCCCCCC 3']. cDNA was
 cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end:
 XhoI. Host: SOIR.

FEATURES

Location/Qualifiers
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 /clone="0610017C21"
 /sex="male"
 /tissue_type="kidney"
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 /dev_stage="adult"
 125..1549
 /note="unnamed protein product; lipoprotein lipase
 (MGD [MG:96820])
 putative"

CDS

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 DSLNEENPSKAYRCNKEAFEGKLCISCRKNCNLGLYEINKVKRKSRSKWLKTRS
 OMPYKVHYQVHKIFSGTDEGKHOQAFEISLYGTVAESENIPFTLPEVSTNKTYSFL
 IYTEVDIGELLMKMLKWTSDSYFSPMDWSSPSFVIERIVKAGETQKVIFCAREKV
 SHLQKGDSDAVFVKCHKSLKKSQ"

ORIGIN

Alignment Scores:			
Pred. No.:	6.01e-247	Length:	2054
Score:	2233.50	Matches:	419
Percent Similarity:	95.98%	Conservative:	11
Best Local Similarity:	93.53%	Mismatches:	17
Query Match:	93.65%	Indels:	1
DB:	3	Gaps:	1

US-10-019-341-3 (1-448) x AK002645 (1-2054)

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QY 21 AspThrAlaGluAspThrCysHisLeuIleProGlyValAlaGluSerValAlaThrCys 40
 Db 266 GACACAGCTGAGGACACTTGTCTCTCATCTCTCTGGATTAGCAGACTCTGTGTCTAATGTC 325

QY 41 HisPheAsnHisSerSerLysThrPheMetValIleHisGlyThrValThrGlyMet 60
 Db 326 CACTTCAACACACAGCAGCAGACCTTCTGTGTGTATCCATGCGGCGGTAAACGGGAATG 385

QY 61 TyrGluSerTyrValProLysLeuValAlaAlaLeuTyrLysArgGluProAspSerAsn 80
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QY 81 ValIleValValAspTyrLeuSerArgAlaGlnGluHisTyrProValSerAlaGlyTyr 100
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QY 101 ThrLysLeuValGlyGlnAspValAlaArgPheIleAsnTyrMetGluGluPheAsn 120
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QY 121 TyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeuGlyValAlaHisAlaGlyIle 140
 Db 566 TACCCCTTAGACAAAGTCCACTCTTAGGTACAGCTTGGAGCCCATCTGCTGCGGTA 625

QY 141 AlaGlySerLeuThrAsnLysLysValAsnArgIleThrGlyLeuAspProAlaGlyPro 160
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 Db 746 GTCTTACACACATTTACAGGGGGTCACTGTGTGGAATTTGGAAATCCAGAAACCGATA 805

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QY 221 AlaIleArgValIleAlaGluArgGlyLeuGlyAspValAspGlnLeuValLysCysSer 240
 Db 866 GCCATCCGTGTGATTGTCAGAGAGAGGACTCGAGACGTGGACCACTGCTGAAGTGTCTG 925

QY 241 HisGluArgSerIleHisLeuPheIleAspSerLeuLeuAsnGluGluAsnProSerLys 260
 Db 926 CACGAGCGCTCCATTCATCTCTTATGACTCCCTGCTGAATGAAGAAACCCAGCAAG 985

QY 261 AlaTyrArgCysSerSerLysGluAlaPheGluLysGlyLeuCysLeuSerCysArgLys 280
 Db 986 GCATACAGTGCACACTCCAGGAAGCCCTTTCAGAAAGGGCTCTGCCTGAGTTGTAGAAAG 1045

QY 281 AsnArgCysAsnAsnLeuGlyTyrGluIleAsnLysValArgAlaLysArgSerSerLys 300
 Db 1046 AATCGCTGTAACTATGGGCTATGAGATCAACAAGGTTCAGAGCAGAGAGAGAGCAAG 1105

QY 301 MetTyrLeuLysThrArgSerGlnMetProTyrLysValPheHisTyrGlnValLysIle 320
 Db 1106 ATGTACCTGAAGACTCCCTCTCAGATGCCCTTACAAAGTGTTCATTACCAAGTCAAGATT 1165

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QY 341 GlyThrValAlaGluSerGluAsnIleProPheThrLeuProGluValSerThrAsnLys 360

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361	ThrTyrSerPheLeuIleTyrThrGluValAspIleGlyLeuLeuMetLeuLysLeu	380
1286	ACCTACTCTCTTGTGATTACACGGAGGTGGACATCGAGAACTGCTCATGATGAAGCTT	1345
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1346	AAAGTGATTAAGCAGCTCTTACTTACCTGAGTGGCTGACTGGTGAGAGCAGCCCGCTTCGTC	1405
401	IleGlnLysIleArgValLysAlaGlyGluThrGlnLysLysValLlePheCysSerArg	420
1406	ATCGAGAGATCCGAGTGAAGGCCGAGAGACTCAGAAAAGGTCATCTTCTGTCTAGG	1465
421	GluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHisAsp	440
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441	LysSerLeuAsnLysLysSerGly	448
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LOCUS	Mus musculus adult female vagina cDNA, RIKEN full-length enriched	
DEFINITION	library, clone:9930034G02 product:lipoprotein lipase, full insert	
ACCESSION	AK079446	
VERSION	AK079446.1 GI:26347994	
KEYWORDS	HTC; CAP trapper.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus; Mus.	
AUTHORS	Carninci, P. and Hayashizaki, Y.	
TITLE	High-efficiency full-length cDNA cloning	
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)	
MEDLINE	99279253	
PUBMED	10349636	
REFERENCE	2	
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)	
MEDLINE	20499374	
PUBMED	11042159	
REFERENCE	3	
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, S., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.	
TITLE	RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer	
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)	
MEDLINE	20530913	
PUBMED	11076861	
REFERENCE	4	
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.	
TITLE	Functional annotation of a full-length mouse cDNA collection	
JOURNAL	Nature 409, 685-690 (2001)	
REFERENCE	5	
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.	
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs	
JOURNAL	Nature 420, 563-573 (2002)	

6 (bases 1 to 2018)
REFERENCE
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanaoka,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitho,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/
FEATURES
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DB	292	TTCAACACAGCAGCAAGACCTTCGTGGTGATCCATGGATGGACGGTAACGGGAATGTAT	351
QY	62	GluSerTrpValProLysLeuValAlaLeuTyrLysArgGluProAspSerAsnVal	81
DB	352	GAGAGTTGGTGCCCAAACTTGTGGCGCCCTGTACAAGAGAACTGACTCCAATGTC	411
QY	82	IleValValAspTrpLeuSerArgAlaGlnGluHisTyrProValSerAlaGlyTyrThr	101
DB	412	ATTGTAGTAGACTGGTTGTATCGGGCCACGACCAATTCACAGTGTCACTGGCTACAC	471
QY	102	LysLeuValGlyClnAspValAlaArgPheIleAsnTrpMetGluGluPheAsnTyr	121
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DB	532	CCCTTAGACAAAGTCCACTCTTAGGTACAGCCTTGAGCCCTGCTCGCGTAGCA	591
QY	142	GlySerLeuThrAsnLysLysValAsnArgIleThrGlyLeuAspProAlaGlyProAsn	161
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QY	222	IleArgValIleAlaGluArgGlyLeuGlyAspValAspGlnLeuValLysCysSerHis	241
DB	832	ATCCGTGTGATTCAGAGAGAGGACTCGGAGCGTGGACCGAGCTGGTGAGTGTCTGCAC	891
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DB	892	GAGCGCTCCATTCACTCTCTCATTTAGCTCCCTGCTGATGAGAAACCCGACGAGCA	951
QY	262	TyrArgCysSerSerLysGluAlaPheGlnLysGlyLeuCysLeuSerCysArgLysAsn	281
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QY	282	ArgCysAsnAsnLeuGlyTyrGluIleAsnLysValArgAlaLysArgSerSerLysMet	301
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QY	302	TyrLeuLysThrArgSerGlnMetProTyrLysValPheHisTyrGlnValLysIleHis	321
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DB	1192	ACAGTGGCCGAGAGCGAACAATTCCTTCACCTCGCCGAGGTTTCCACAAATAAAACC	1251
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DB	1252	TACTCTCTTGTATTACACGGAGGTGGACATCGGAGAACTGCTCATGATGAAGCTTAAG	1311
QY	382	TrpLysSerAspSerTyrPheSerTrpSerAspTrpTrpSerSerProGlyPheAlaIle	401

Db	1312	TGGATAAGCGACTCTTACTTCAGTGCGCCTGACTGTGGAGCAGCCACGCTCGTCATC	
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Db	1372	GAGAGATCCGAGTGAAGCCGAGAGACTCAGAAAAGGTCATCTTCTGTGCTGGGAG	
QY	422	LysValSerHisLeuGlnLysGlyLyAlaProAlaValPheVallylscySHisAspLys	
Db	1432	AAAGTTTCTCATCTGCAGAAGGGAAGCACTCAGCAGTGTTTGTGAATGCCATGACAAG	
QY	442	SerIeuAenLysLysSergly	448
Db	1492	TCTCTG---AAGAAGTCTGGC	1509
RESULT 7			
LOCUS	AKO17272	Mus musculus 6 days neonate head cDNA, RIKEN full-length enriched library, clone:5430405H20 product:lipo-protein lipase, full insert sequence.	1899 bp mRNA linear HTC 03-APR-2004
DEFINITION			
ACCESSION	AKO17272		
VERSION	AKO17272.1	GI:12856426	
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;		
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
MEDLINE	20499374		
PUBMED	11042159		
REFERENCE	Shibata, K., Itoh, M., Aizawa, K., Nagao, K., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsumai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watakabe, K., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuda, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.		
AUTHORS	RIKEN Integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multipipette sequencer		
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)		
MEDLINE	20530913		
PUBMED	11076861		
REFERENCE	Shibata, K., Itoh, M., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Katoh, C., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Kosuga, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Katoh, C., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Kosuga, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K.		
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.		
TITLE	Functional annotation of a full-length mouse cDNA collection		
JOURNAL	Nature 409, 695-699 (2001)		
REFERENCE	Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Katoh, C., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Kosuga, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K.		
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.		
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs		
JOURNAL	Nature 420, 563-573 (2002)		
REFERENCE	(bases 1 to 1899)		

Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C.,
 Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D.,
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 Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T.,
 Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K.,
 Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
 Direct Submission
 Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,
 URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
 Fax: 81-45-503-9216)
 please visit our web site (http://genome.gsc.riken.jp/) for further
 details.
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues. First strand cDNA was primed with a primer
 [5', GAGAGAGAGATCCAGAGCTCTTTTCTTTTNN 3'], cDNA was
 prepared by using trihalose thermo-activated reverse transcriptase
 and subsequently enriched for full-length by cap-trapper. cDNA went
 through one round of normalization to Rot = 10.0 and subtraction to
 Rot = 100.0. Second strand cDNA was prepared with the primer
 adapter of sequence [5'
 GAGAGAGAGATCTCGAGTTAAATTAATCCGCCGCCGCC 3']. cDNA was cleaved
 with BamHI and XhoI. Vector: a modified pBluescript KS(+) after
 bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3'
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 putative"

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 DB 1478 ATCAGAGAGTCCAGGTGAAGCCGAGAGACTCAGAAAAGGTCATCTTCTGTGCTAGG 1537
 QY 421 GluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheValLysCysHisAsp 440
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ACCESSION AY410290
VERSION   AY410290.1 GI:39766258
KEYWORDS  GSS.
SOURCE    Pan troglodytes (chimpanzee)
ORGANISM  Pan troglodytes
REFERENCE 1 (bases 1 to 1427)
AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL   Science 302 (5652), 1960-1963 (2003)
PUBMED    14671302
REFERENCE 2 (bases 1 to 1427)
AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE     Direct Submission
JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT   This sequence was made by sequencing genomic exons and ordering them based on alignment.
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Best Local Similarity: 79.46%      Mismatches:  91
Query Match:    76.90%      Indels:      0
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue
2 (bases 1 to 2791)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
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ACCESSION AL539198
VERSION AL539198.3 GI:45714871
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1063)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:31263768.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 4684.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS0DF034YK01&c=4684.f.
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ORIGIN

Alignment Scores:
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US-10-019-341-3 (1-448) x AL539198 (1-1063)

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QY 197 GlnLysProValGlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGlyCys 216
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 DB 243 GTGAAGTGTCTCCACAGAGCTCCATTCATCTCTTCATCGACTCTCTGTGATGAGAA 302

QY 257 AsnProSerLysAlaTyrArgCysSerSerLysGluAlaPheGluLysGlyLeuCysLeu 276
 DB 303 AATCCAGTAAAGCTTACAGGTGCGAGTCCAAAGGAGCCTTTGAGAAAGGCTCTGCTTG 362

QY 277 SerCysArgLysAsnArgCysAsnLeuGlyTyrGluIleAsnLysValArgAlaLys 296
 DB 363 AGTTGTAGAAAGAACCGCTGCAACATCTGGCTATGATGATCAATTAAGTCAGACCCAAA 422

QY 297 ArgSerSerLysMetTyrLeuLysThrArgSerGlnMetProTyrLysValPheHisTyr 316
 DB 423 AGAAGCAGCAAAATGTACTGAAGACTCGTTCTCAGATGCCCTACAAAGTCTTCCATTAC 482

QY 317 GlnValLysIleHisPheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPheGlu 336
 DB 483 CAAGTAAAGATTCATTTTCTGGAGCTGAGAGTGAACCCATACCAATCAGGCTTTGAG 542

QY 337 IleSerLeuTyrGlyThrValAla-GluSerGluAsnIleProPheThrLeuProGluVa 356
 DB 543 ATTTCTCTGTATGCACCGTGGCGAGGTGAGACATCCCATTCATCTCTGCTGAGT 602

QY 356 lSerThrAsnLysThrTyrSerPheLeuIleTyrThrGluValAspIleGlyGluLeuLe 376
 DB 603 TTCCACAAATWAGACCTACTCTCTCTTAATTTACACAGAGGTAGATATTGGAGAACTACT 662

QY 376 uMetLeuLysLeuLysTrpLysSerAspSerTyrPheSerTrpSerAspTrpTrpSerSe 396
 DB 663 CATGTTGAGCTCAATGGAAGATGATTCATCTTTAGCTGGTGGAGTGGAGCAG 722

QY 396 rProGlyPheAlaIleGlnLysIleArgValLysAlaGlyGluThrGlnLysLysValI 416
 DB 723 TCCGGGCTTCGCCATTTCAGAGATCAGATTAAGACGAGGAGACTCAGAAAAAGGTGAT 782

QY 416 ePheCysSerArgGlnLysValSerHisLeuGlnLysGlyLysAlaProAlaValPheVa 436

Db 783 CTTCTGTTCTAGGAGAAAGTGTCTCATTTGACAGAAAGAAAGCACCTGGGTATTGT 842

Qy 436 lLysCysHisAspLysSerLeuAsnLysLysSerGly 448
 Db 843 GAAATGCCATGACAAAGTCTCTGAAATAGAAAGTCAAGC 879

RESULT 11
 BX418566
 LOCUS
 DEFINITION BX418566 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
 CS0DF007YI16 5-PRIME, mRNA sequence.
 ACCESSION BX418566
 VERSION BX418566.2 GI:46927755
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 JOURNAL 1. (bases 1 to 1076)
 COMMENT Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On May 13, 2003 this sequence version replaced gi:30642295.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
 was not normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 This sequence belongs to sequence cluster 4684.f
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?s=CS0DF007BE080P1sc=4684.f.
 Location/Qualifiers
 1..1076
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DF007YI16"
 /tissue_type="FETAL BRAIN"
 /dev_stage="fetal"
 /clone_lib="Homo sapiens FETAL BRAIN"
 /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
 was primed with a NotI-oligo (dT) primer. Five prime end
 enriched, double-strand cDNA was digested with Not I and
 cloned into the Not I and EcoRV sites of the pCMVSPORT 6
 vector. Library was not normalized."

FEATURES

source

ORIGIN

Alignment Scores:
 Pred. No.: 4,2e-158 Length: 1076
 Score: 1463.00 Matches: 277
 Percent Similarity: 95.59% Conservative: 5
 Best Local Similarity: 93.90% Mismatches: 13
 Query Match: 61.34% Indels: 1
 DB: 5 Gaps: 0

US-10-019-341-3 (1-448) x BX418566 (1-1076)

Qy 154 GlyLeuAspProAlaGlyProAsnGlyThrAlaGluAlaProSerArgLeuSerPro 173
 Db 1 GGCTCGATCCAGCTGGACCTACTTTCAGTATGACAGAGCCCGAGTCGTTCTCTCT 60

Qy 174 AspAspAlaAspPheValAspValLeuHisThrPheThrArgGlySerProGlyArgSer 193
 Db 61 GATGATGCAGATTTGTAGACGCTTACACATTCACAGAGGGTCCCTGGTCGAGC 120

Qy 194 lLysGlyLeuGlnLysProValGlyHisValAspIleTyrProAsnGlyGlyThrPheGln 213
 Db 121 ATTGGAATCCAGAAACAGTTGGGCATGTTGACATTTACCCGAATGAGGTACTTTTCAG 180

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: NDAM618 row: h column: 05
 High quality sequence stop: 701.
 Location/Qualifiers
 1. 877
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30529996"
 /lab_host="DH10B-Tona (71 and T5 phage resistant)"
 /clone_lib="NIH MGC 183"
 /note="Organ: Pooled muscle (cardiac and skeletal); Vector: pCMV-SPORT6.1; Site 1: EcoRV (destroyed); Site 2: NotI; Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7. Library was constructed by Invitrogen."

FEATURES

source

ORIGIN

Alignment Scores:

Pred. No.: 1,49e-149 Length: 877
 Score: 1388.00 Matches: 270
 Percent Similarity: 99.27% Conservatives: 1
 Best Local Similarity: 98.90% Mismatches: 2
 Query Match: 58.20% Indels: 2
 DB: 7 Gaps: 0

US-10-019-341-3 (1-448) x CF551983 (1-877)

214 ProGlyCysAsnIleGlyGluAlaIleArgValIleAlaGluArgGlyLeuGlyAspVal 233
 Db 181 CCAGATGTACATTTGGAGAGCTATCCGCGTGATTCAGAGAGAGGACTTGGAGATGTG 240
 Qy 234 AspGlnLeuValLysCysSerHisGluArgSerIleHisLeuPheIleAspSerLeuLeu 253
 Db 241 GACCAGCTAGTGAAGTGTCTCCACGAGCGCTCCATTCATCTCTTCATGACTCTCTTTT 300
 Qy 254 AsnGluGluAenProSerLysAlaTyrArgCysSerSerLysGluAlaPheGluLysGly 273
 Db 301 AATAAAAAAATCCCAAGTAAAGCCCTACAGTGCAGTTCACAGGAGCCCTTTGARAAGGG 360
 Qy 274 LeuCysLeuSerCysArgLysAsnArgCysAenAenLeuGlyTyrGluIleAsnLysVal 293
 Db 361 CTCGCTTGAATGTAGAAAGAACCGCTGCAACAATCTGGGTATGAAATCAATAAATC 420
 Qy 294 ArgAlaLysArgSerSerLysMetTyrLeuLysThrArgSerGlnMetProTyrLysVal 313
 Db 421 AGAGCCAAAAAAGAGCAGCAAAATGTACCTGAAAGATCTGTTCTCAGATGCCCTACAAAGTC 480
 Qy 314 PheHisTyrGlnValLysIleHisPheSerGlyThrGluSerGluThrHisThrAenGln 333
 Db 481 TTCATTACCAAGTAAAGATTCATTTCTGGAGCTGAGAGTGAAACCCATACCAATCAG 540
 Qy 334 AlaPheGluIleSerLeuTyrGlyThrValAlaGluSerGluAsnIleProPheThrLeu 353
 Db 541 GCCTTTAAATTTCTCTGTATGCACCGTGGCGGAGAGTGAGAACCATCCATTCACACTCG 600
 Qy 354 ProGluValSerThrAsnLysThrTyrSerPheLeuIleTyrThrGluValAspIleGly 373
 Db 601 CCGTGAAGTTTCACAAATTAAGACTTACTCTCTCTTAATTTACACAGGAGGAGATTTGGA 660
 Qy 374 GluLeuLeuMetLeuLysLysTyrLysSerAspSerTyrPheSerTrpSerAspTrp 393
 Db 661 GAACACTACTCATGTTGAAGTCAATATGAGAGATGATTCATATTTAGCTGGKAGACTGG 720
 Qy 394 TrpSerSerProGlyPheAlaIleGlnLysIleArgValLysAlaGlyGluThrGlnLys 413
 Db 721 TGGRCGAGTCCCGGTTGCG-ATTCAAGATCAGAGTAAATCAAGAGAGACTCAGAA 779
 Qy 414 LysValIlePheCysSerArgGluLysValSerHisLeuGlnLysGlyLysAlaProAla 433
 Db 780 AAGGTGATCTCTGTTTATAGGGGAAAGTGTCTCATTTGCAAGAGAGAGGRCCTGCG 839
 Qy 434 ValPheValLysCysHisAspLysSerLeuAsnLysLysSerGly 448
 Db 840 GKATTTTGAAATGCCATGACAGTCTCTGTAATAAAGTCAGGG 884

RESULT 12

CF551983 877 bp mRNA linear EST 22-SEP-2003
 LOCUS AGENCOURT 15594985 NIH MGC 183 Homo sapiens cDNA clone
 DEFINITION IMAGE:30529996 5', mRNA sequence.

ACCSSION CF551983

VERSION CF551983.1 GI:34888817

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 877)

NIH-MGC <http://mgs.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapsb-r@mail.nih.gov

Tissue Procurement: Dr. Michael Brownstein

cDNA Library Preparation: Invitrogen Corp

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

176 AlaAspPheValAspValLeuHisThrPheThrArgGlySerProGlyArgSerIleGly 195
 Db 1 GCAGATTTTGTAGAGCTCTTATC-ACATTCACAGAGGGTCCCTGTCGAGCATTTGA 59
 Qy 196 IleGlnLysProValGlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGly 215
 Db 60 ATCCAGAAACCAAGTTCGGCATCTTGACATTTACCCCAATGGAGGTACTTTTCAGCCAGGA 119
 Qy 216 CysAsnIleGlyGluAlaIleArgValIleAlaGluArgGlyLeuGlyAspValAspGln 235
 Db 120 TGTAAATTTGGAGAGCATATCCCGTGATTCAGAGAGAGGAGACTTGGAGATGTGGACAG 179
 Qy 236 LeuValLysCysSerHisGluArgSerIleHisLeuPheIleAspSerLeuLeuAsnGlu 255
 Db 180 CTAGTGAAGTGTCTCCACAGAGCGCTCCATTCATCTCTTCATGACTCTCTGTTGAATGAA 239
 Qy 256 GluAsnProSerLysAlaTyrArgCysSerSerLysGluAlaPheGluLysGlyLeuCys 275
 Db 240 GAAAAATCCAAAGTAAGGCTACAGGTGCAGTTCACAGGAGGCTTTTGAGAAAGGCTCTGC 299
 Qy 276 LeuSerCysArgLysAsnArgCysAsnLeuGlyTyrGluIleAsnLysValArgAla 295
 Db 300 TTGAGTTGTAGAAAGAACCCCTGCAACAATCTGGCTATGAGATCAATAAAGTCAGAGCC 359
 Qy 296 LysArgSerSerLysMetTyrLeuLysThrArgSerGlnMetProTyrLysValPheHis 315
 Db 360 AAAAGAGAGCAGCAAAATGTACCTGAGAGCTCGTTCTCAGATGCCCTCAAAAGTCTTCAT 419
 Qy 316 TyrGlnValLysIleHisPheSerGlyThrGluSerGluThrHisThrAsnGlnAlaPhe 335
 Db 420 TACCAAGTAAAGATTCATTTTCTGGGACTGAGAGTGAACCCATACCAATCAGGCGCTTT 479
 Qy 336 GluIleSerLeuTyrGlyThrValAlaGluSerGluAsnIleProPheThrLeuProGlu 355
 Db 480 GAGATTTCTGTATGGCACCCTGGCCGAGAGTGAACATCCCATTCACCTCTGCTGAA 539
 Qy 356 ValSerThrAsnLysThrTyrSerPheLeuIleTyrThrGluValAspIleGlyGluLeu 375
 Db 540 GTTTCCCAAAATAAGACCTACTCTCTTCTTAATTTACACAGAGGTAGATTATGGAGAACTA 599
 Qy 376 LeuMetLeuLysLeuLysTrpLysSerAspSerTyrPheSerTrpSerAspTrpSer 395
 Db 600 CTCATGTTGAAGCTCAAAATGGAAGAGTGAATTCATCTTTAGCTGCTCAGACTGGTGGAGC 659

QY 396 SerProGlyPheAlaIleGlnLysIleArgValLysAlaGlyGluThrGlnLysVal 415
 Db 660 AGTCCCGGCTTCGCAATCAGAGATCAGATAAGCAGAGAGATCTCAGAAAAAGGTG 719
 QY 416 IlePheCysSerArgGluLysValSerHisLeuGlnLysGlyLysAlaProAlaValPhe 435
 Db 720 ATCTCTGTTCTAGGAGAAAGTGTCTCATTTGCAGAAAGGAAAGCA-CTGCGGTATTT 778
 QY 436 ValLysCysHisAspLysSerLeuAsnLysSerGly 448
 Db 779 GTGAATGCCATGACAAAGTCTCTGAATAAGAAAGTCAGGC 817

RESULT 13
 CO734715 812 bp mRNA linear EST 29-JUL-2004
 LOCUS SLH03C09j06f1 squirrel heart library 1 Spermophilus lateralis cDNA
 DEFINITION clone 09j06 5', mRNA sequence.

ACCESSION CO734715
 VERSION
 KEYWORDS
 SOURCE

ORGANISM Spermophilus lateralis (golden-mantled ground squirrel)
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Scuridae; Scurinae;
 Spermophilus.

REFERENCE 1 (bases 1 to 812)
 AUTHORS Williams,D.R., Gracey,A.Y., Martin,S.L., Hughes,M.A., Li,W.,
 Rogers,J. and Cossins,A.R.
 TITLE Microarray analysis of transcriptional changes during hibernation
 JOURNAL in the golden mantled ground squirrel, Spermophilus lateralis
 COMMENT Unpublished (2004)
 Contact: Andrew R. Cossins
 Laboratory for Environmental Gene Regulation
 University of Liverpool
 School of Biological Sciences, The Biosciences Building, Crown
 Street, Liverpool, United Kingdom, L69 7ZB
 Tel: +44(0)151-795-4510
 Fax: +44(0)151-795-4431
 Email: cossins@liv.ac.uk
 Vector has been trimmed from this EST.
 Plate: 09 row: j column: 06
 Seq primer: pf1c T7 (5'-AATACGACTCACTATAGG-3')
 High quality sequence stop: 812.

FEATURES
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 1..812
 /organism="Spermophilus lateralis"
 /mol_type="mRNA"
 /db_xref="taxon:76772"
 /clone="09j06"
 /sex="Male & female"
 /tissue_type="Heart"
 /dev_stage="Adult"
 /lab_host="E.coli Electromax DH10B"
 /clone_lib="squirrel heart library 1"
 /note="Vector: pFLC; Site 1: SalI GTCGAG; Site 2: BamHI
 GGATCC; Normalized and subtracted cDNA library prepared
 from heart of hibernating and summer animals"

ORIGIN
 Alignment Scores:
 Pred. No.: 4.33e-137 Length: 812
 Score: 1280.00 Matches: 241
 Percent Similarity: 97.25% Conservative: 7
 Best Local Similarity: 94.51% Mismatches: 6
 Query Match: 53.67% Indels: 1
 DB: 7 Gaps: 0

US-10-019-341-3 (1-448) x CO734715 (1-812)

QY 1 AlaAspGlnArgAspPheIleAspIleGluSerLysPheAlaLeuArgThrProGlu 20
 Db 49 GCTCCGACGCAAGAGAGTTAAGGACATCGAAAGTAATTTGCCCTAAGGACTCTGAA 108

QY 21 AspThrAlaGluAspThrCysHisLeuIleProGlyValAlaGluSerValAlaThrCys 40
 Db 109 GACACAGCTGAGGACACTTCCCACTGCTTCTCGAGTGTGAGAGTCTGTGGCCACTGC 168
 QY 41 HisPheAsnHisSerSerLysThrPheMetValIleHisGlyThrThrValThrGlyMet 60
 Db 169 CACTTCAACACACAGCAGCAAGACCTTCGTGTGTATCCACGCTGGACGGTGACAGGATG 228
 QY 61 TyrGluSerTrpValProLysLeuValAlaAlaLeuTyrLysArgGluProAspSerAsn 80
 Db 229 TATGAGAGTTGGGTGCCAAACTTGTGGCTGCTTGTATAGAGGGAAACCGGACTCCAAC 288
 QY 81 ValIleValValAspTrpLeuSerArgAlaGlnGluHisTyrProValSerAlaGlyTyr 100
 Db 289 GTCATCGTGTGACTGGCTGTGCGGGCCACAGCAGCATTTACCGGTGTCTGAGGCTAC 348
 QY 101 ThrLysLeuValGlyGlnAspValAlaArgPheIleAsnTrpMetGluGluGluPheAsn 120
 Db 349 ACCAAGCTGTGTGGAAAGGATGTGGCCAGATTTTCACTGGATGGAGGAGGAATTTAAC 408
 QY 121 TyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeuGlyAlaHisAlaGlyIle 140
 Db 409 TACCTGTGGACAACTCCATCTCTTGGGATACAGCTTGGAGCCCATGCGCTGGCATT 468
 QY 141 AlaGlySerLeuThrAsnLysLysValAsnArgIleThrGlyLeuAspProAlaGlyPro 160
 Db 469 GCAGGAAGTCTGACCAATTAAGAAAGTCAACAGATTTACTGGCTGGACCCAGCTGGACCT 528
 QY 161 AsnPheGluTyrAlaGluAlaProSerArgLeuSerProAspAlaAspPheValAsp 180
 Db 529 AACTTTGAGTATGCAGAGCTCTCTAGCCGCTTCTCTCTGATGATCGGATTTCTGTAGAC 588
 QY 181 ValLeuHisThrPheThrArgGlySerProGlyArgSerIleGlyIleGlnLysProVal 200
 Db 589 GTCTTACACAGCTTACACAGAGGCTCTCGGATAGAGATTTGGGATTCAGAGCCAGTA 648
 QY 201 GlyHisValAspIleTyrProAsnGlyGlyThrPheGlnProGlyCysAsnIleGlyGlu 220
 Db 649 GGGCAGCTTGATATTATTTACCCCAATGGAGGCACTTTTCAACACAGGATGCACATTTGGGAA 708
 QY 221 AlaIleArgValIleAlaGluArgGlyLeuGlyAspValAspGln-LeuValLysCysSe 240
 Db 709 GCTATTCTGTGTAATTCAGAGAGAGGCTTGGAGATGTGGACGACGCTGTGAAGTCTC 768
 QY 240 HisGluArgSerIleHisLeuPheIleAspSerLeuLeuAsn 254
 Db 769 CCATGAGCGCTCCATTCATCTCTTCATCGACTCCCTGTGTAAT 811

RESULT 14
 BI599196 896 bp mRNA linear EST 07-SEP-2001
 LOCUS 03250225F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5301799 5',
 DEFINITION mRNA sequence.
 ACCESSION BI599196
 VERSION BI599196.1 GI:15492135
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 896)
 NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgsb@robert.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
 Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LHAM11764 row: b column: 08 High quality sequence stop: 805.	
FEATURES	Location/Qualifiers
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	/clone="IMAGE:5301799"
	/tissue_type="hypothalamus"
	/lab_host="DH10B"
	/clone_lib="NIH_MGC_96"
	/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcagag); Oligo-dT primed using primer 5'-TTTTTTTTTTTNN-3', size-selected for average insert size 2.3 kb and normalized to 80T 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
ORIGIN	
Alignment Scores:	
Pred. No.:	2.2e-136 Length: 896
Score:	1274.50 Matches: 265
Percent Similarity:	93.40% Conservative: 4
Best Local Similarity:	92.01% Mismatches: 11
Query Match:	53.44% Indels: 10
DB:	4 Gaps: 1
US-10-019-341-3 (1-448) x B1599196 (1-896)	
QY	1 AlaAspGlnArgAspPheHisLeuSerHisPheAlaLeuArgThrProGlu 20
DB	51 GCCGCCAAGAAGAGATTATTCGACATCGAAGTAATTTGCCCTTAGACCCCTGAA 110
QY	21 AspThrAlaGluAspThrCysHisLeuLeuProGly-ValAlaGluSerValAlaThrCy 40
DB	111 GACACAGCTGAGACACTTCCACCTCATTTCCCGAGATAGCAGAGTCCATGCTACCTG 170
QY	40 sHisPheAsnHis-SerSerHisThrPheMetValHisGlyThrValThrGlyM 60
DB	171 TCATTTCAATCACAGACAGCAAAACCTTCATGTTGATCCATGCTGACCGGTAAACGAA 230
QY	60 etTyrGluSerTrpValProLysLeuValAlaLeuTyrLysArgGluProAspSerA 80
DB	231 TGTATGAGATTGGTGCCAAAACCTTGTGCGCCCTGTACAGAGAACACGACTCCA 290
QY	80 snValLeuValAspTrpLeuSerArgAlaGlnGluHisTyrProValSerAlaGlyT 100
DB	291 ATGTCATTGTTGGTGGCTGCTGCACGGGC-CAGGAGCATTTACCCAGTGTCCCGGGCT 349
QY	100 YrThrLysLeuValGlyGlnAspValAlaArgPheHisLeuSerLeuGluGluPheA 120
DB	350 ACACCAACTGTTGGCAGCAGGATGGCCCGGTTTATCACTGGATGGAGGAGGTTTA 409
QY	120 snTyrProLeuAspAsnValHisLeuLeuGlyTyrSerLeuGlyValaHisAlaGlyI 140
DB	410 ACTACCTCTCGCAAGATGTCATCTCTGGATACAGCTTGGAGCCCATGCTCTGGCA 469
QY	140 leAlaGlySerLeuThrAsnLysLysValAsnArgIleThrGlyLeuAsp-ProAlaGly 159
DB	470 TTGCAGAGAGTCTGACCAATAAGAAAGTCAACAGAAATTAATCTGCTGATCCAGCTGA 529
QY	160 ProAsnPheGluTyrAlaGluAlaProSerArgLeuSerProAspAspAlaAspPheVal 179
DB	530 CCTAACTTGTAGTATGACAGACCCCGAGTGGTCTTCTCTGTGATGTCAGATTTGTA 589
QY	180 AspValLeuHisThrPheThrArgGlySerProGlyArgSerIleGlyIleGlnLysPro 199
Db	590 GACGCTTTACACACATTCCACGAGGGTCCCTGGTGGAGCATTTGGAAATCCAGAAACCA 649
QY	200 ValGlyHisValAspIleTyrProAsnGlyGlyThrPheGlnPro-GlyCysAsnIleGl 219
DB	650 GTTGGGCATGTTGACATTTACCCGAATGGAGTACTTTTTCAGCCAGGATGTAAACATTGG 709
QY	219 yGluAlaIleArgValIleAlaGluArg-GlyLeuGlyAspVal-AspGlnLeuValLys 238
DB	710 AGAGCTATCCGGGTGATTCCGAGAGAAGGACTTGGCGATGTTGGACCCAGCTAGTGAAG 769
QY	239 Cys-SerHisGluArgSerIleHisLeuPheIleAspSerLeuLeuAsnGluGluAsnPr 258
DB	770 TGGCTCCACAGAGCGCTCCATTCATCTCTTCATCGACTCTCTGTGTAATGGAGAAATCC 829
QY	258 oSerLysAlaTyrArgCysSerSerLysGluAlaPheGluLysGlyLeuCysLeuSerCy 278
DB	830 AGTGAAGCGCTACAGGTGCCG-TCCAGGAGGCCCTTGGAAAAGGGG---CCGTGGAAGTG 885
QY	278 sArgLysAsn 281
DB	886 TCAAGAAAC 895
RESULT 15	
CO557716	
LOCUS	800 bp mRNA linear EST 19-JUL-2004
DEFINITION	AGENCOURT 28460550 NIH_MGC 248 Rattus norvegicus cDNA clone
ACCESSION	IMAGE:7365245 5', mRNA_sequence.
VERSION	CO557716
KEYWORDS	CO557716.1 GI:50370260
SOURCE	EST.
ORGANISM	Rattus norvegicus (Norway rat)
	Rattus norvegicus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
	Rattus.
REFERENCE	1 (bases 1 to 800)
AUTHORS	NIH-MGC http://img.nci.nih.gov/.
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892 Email: cgraphs@mail.nih.gov Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical College of Wisconsin cDNA Library Preparation: Open Biosystems cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LHAM15499 row: g column: 03 High quality sequence start: 5 High quality sequence stop: 694.
FEATURES	Location/Qualifiers
source	1..800
	/organism="Rattus norvegicus"
	/mol_type="mRNA"
	/db_xref="taxon:10116"
	/clone="IMAGE:7365245"
	/lab_host="DH10B Tona"
	/clone_lib="NIH_MGC_248"
	/note="Organ: spleen; Vector: pExpress-1; Site 1: EcoRV; Site 2: NotI; RNA obtained from testis tissue of 8 wk old animal. Tissues were snap-frozen and kept at -80C before RNA extraction and purification (TRI-reagent method). cDNA was primed using oligo-dT primer: 5'-pGACTAGTCTAGATCGAGCGCCGCC(T)25-3' and cloned into the EcoRV/NotI sites of pExpress-1. Size-selection >1.25kb resulted in an average insert size of 1.7 kb. This is a primary library (normalized library is NIH_MGC_249) and was constructed by Open Biosystems. Note: this is a NIH_MGC

```

ORIGIN
Library*

Alignment Scores:
Pred. No.:      1e-134      Length:      800
Score:          1259.50     Matches:    237
Percent Similarity: 96.84%   Conservative: 8
Best Local Similarity: 93.68% Mismatches:    7
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

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(without alignments)
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Searched: 4526729 seqs, 23644849745 residues

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Listing first 45 summaries

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Result No. Score Match Length DB ID Description

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1
HSLIPAS
LOCUS Human mRNA for lipoprotein lipase (EC 3.1.1.34).
DEFINITION
ACCESSION X54516
VERSION X54516.1 GI:34382
KEYWORDS Lipase; lipoprotein lipase.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1612)
AUTHORS Takagi, A., Ikeda, Y. and Yamamoto, A.
TITLE DNA sequence of lipoprotein lipase cDNA cloned from human monocytic leukemia THP-1 cells
JOURNAL Nucleic Acids Res. 18 (21), 6436 (1990)
MEDLINE 91057142
PUBMED 2243796
REFERENCE 2 (bases 1 to 1612)
AUTHORS Takagi, A.
TITLE Direct Submission
JOURNAL Submitted (28-AUG-1990) Takagi A., National Cardiovascular Center Research Institute, Dept of Etiology and Pathophysiology, 5-7-1 Fujishirodai Suita, Osaka 565, Japan
COMMENT Data kindly reviewed (04-DEC-1990) by Takagi A.
FEATURES Location/Qualifiers
source
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/organism="Homo sapiens"

ALIGNMENTS

LOCUS	HSLIPAS	Human mRNA for lipoprotein lipase (EC 3.1.1.34).	1612 bp	mRNA	linear	PRI 23-MAR-1995
DEFINITION	Human mRNA for lipoprotein lipase (EC 3.1.1.34).					
ACCESSION	X54516					
VERSION	X54516.1	GI:34382				
KEYWORDS	Lipase; lipoprotein lipase.					
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ORGANISM	Homo sapiens					
REFERENCE	1 (bases 1 to 1612)					
AUTHORS	Takagi, A., Ikeda, Y. and Yamamoto, A.					
TITLE	DNA sequence of lipoprotein lipase cDNA cloned from human monocytic leukemia THP-1 cells					
JOURNAL	Nucleic Acids Res. 18 (21), 6436 (1990)					
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AUTHORS	Takagi, A.					
TITLE	Direct Submission					
JOURNAL	Submitted (28-AUG-1990) Takagi A., National Cardiovascular Center Research Institute, Dept of Etiology and Pathophysiology, 5-7-1 Fujishirodai Suita, Osaka 565, Japan					
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Query Match: 100.00% Indels: 0
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RESULT 2
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ACCESSION X14390
VERSION X14390.1 GI:34404
KEYWORDS lipoprotein lipase.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1924)
REFERENCE
AUTHORS Gotoda,T., Senda,M., Gamou,T., Furuichi,Y. and Oka,K.
TITLE Nucleotide sequence of human cDNA coding for a lipoprotein lipase
(LPL) cloned from placental cDNA library
JOURNAL Nucleic Acids Res. 17 (6), 2351 (1989)
MEDLINE 89202044

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PUBMED 2701938
REFERENCE 2 (bases 1 to 1924)
AUTHORS Senda,M.
TITLE Direct Submission
JOURNAL Nippon Roche Research Center, 200 Kaziwara Kamakura shi, Kanagawa
COMMENT The sequence overlaps with that reported by Wion et. al. in Science
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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RESULT 3

AK092286

LOCUS

DEFINITION

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Mon Oct 25 15:42:52 2004

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AK092286.1 GI:21750843
oligo capping; fis (full insert sequence).

KEYWORDS
SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE

AUTHORS

1 Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R.,
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Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M.,
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Inagaki, H., Ikema, Y., Okamoto, S., Senba, T., Matsumura, K.,
Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Matsumura, K.,
Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T.,
Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima, S.,
Sato, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K.,
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Complete sequencing and characterization of 21,243 full-length
human cDNAs
Nat. Genet. 36 (1), 40-45 (2004)
14702039

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

2 Ninomiya, K., Wagatsuma, M., Kanda, K., Kondo, H., Yokoi, T.,
Kodaira, H., Furuya, T., Takahashi, M., Kikkawa, E., Omura, Y., Abe, K.,
Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M.,
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Yamamoto, J., Isono, Y., Kawai, H., Saito, K., Nishikawa, T.,
Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M.,
Kikuchi, H., Murakawa, K., Kanehori, K., Takahashi, F.,
Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S.,
Nagahara, K., Masuho, Y., Nagai, K. and Isogai, T.
NEDO human cDNA sequencing project
Unpublished
3 (bases 1 to 2385)

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

Isogai, T. and Yamamoto, J.
Direct Submission
Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamata, Kisarazu, Chiba 293-0812, Japan
(E-mail: genomics@kri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
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source

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REFERENCE 1
AUTHORS    Kober, I., Albers, M., Koegl, M., Blume, B., Deuschle, U. and
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us-10-019-341-3.rge

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VERSION CQ720002.1 GI:42280859
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
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thereof
JOURNAL Patent: WO 02068579-A 5936 06-SEP-2002;
PE Corporation (NY) (US)
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PAUI8091

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

PAUI8091 3563 bp mRNA linear PRI 14-SEP-1995
 Papio anubis lipoprotein lipase mRNA, complete cds.
 U18091
 U18091.1 GI:602295

Papio anubis (olive baboon)

Papio anubis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

Cercopithecoidea; Papio.

1 (bases 1 to 3563)

Cole, S.A. and Hixson, J.E.

Baboon lipoprotein lipase: cDNA sequence and variable

tissue-specific expression of two transcripts

Gene 161 (2), 265-269 (1995)

95394368

7665091

REFERENCE	2 (bases 1 to 3563)	
AUTHORS	Cole, S.A.	
TITLE	Direct Submission	
JOURNAL	Submitted (04-DEC-1994) Shelley A. Cole, Genetics, Southwest Foundation for Biomedical Research, P.O. Box 28147, San Antonio, TX 78228-0147, USA	
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AUTHORS	Kainine, N., Chen, X., Rolfs, A., Halleck, A., Hines, L., Eisenstein, S., Koundinya, M., Raphael, J., Moreira, D., Kelley, T., LaBaer, J., Lin, Y.,	

Phelan, M. and Farmer, A.
Cloning of human full-length CDSs in BD Creator (TM) System Donor
vector
Unpublished
2 (bases 1 to 1428)
Kalline, N., Chen, X., Rolfs, A., Halleck, A., Hines, L., Eisenstein, S.,
Koundinya, M., Raphael, J., Moreira, D., Kelley, T., Labaer, J., Lin, Y.,
Phelan, M. and Farmer, A.
Direct Submission
Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow
Circle, Palo Alto, CA 94303, USA
This CDS clone is a part of a collection of human full length
expression clones generated by BD Biosciences Clontech and the
Harvard Institute of Proteomics. Each CDS has been cloned in two
forms: with and without stop-codon (to allow fusion with C-terminal
tag). The CDS has been directionally cloned using BD In-Fusion (TM)
cloning system between the SalI and HindIII sites of the pDNR-DUAL
vector. Additional sequences in the clone: 'ACC' after SalI site
and before 'ATG' to provide Kozak consensus sequence; 'GG' after
last codon and before HindIII site to maintain reading frame.
Clone distribution: <http://bioinfo.clontech.com/orfclones>.

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Mon Oct 25 15:42:52 2004

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BC011353

LOCUS

DEFINITION

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Homo sapiens

Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: amg@bcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
 Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, R.G., Nanavati,
 A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
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ORIGIN

Alignment Scores:

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US-10-019-341-3 (1-448) x BC011353 (1-2315)

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PROC. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 12477932

2 (bases 1 to 2315)

Strausberg,R.

Direct Submission

Submitted (25-JUL-2001)

National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapb-r@mail.nih.gov

Tissue Procurement: David N. Louis, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Baylor College of Medicine Human Genome

Sequencing Center

Center code: BCM-HGSC

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

REMARK

COMMENT

Db 1463 AAGTCTCTGATGAAGAAGTCAGGC 1486

RESULT 13

CR457054

LOCUS

DEFINITION

SOURCE

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

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CR457054 1428 bp mRNA linear PRI 03-JUN-2004
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 gene LPL, lipoprotein lipase; complete cds, incl. stopcodon.

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gene

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ORIGIN

Alignment Scores:

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Query Match:	99.41%	Indels:	0
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US-10-019-341-3 (1-448) x CR457054 (1-1428)

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QY	401	IleGlnLysIleArgValLysAlaGlyGluThrGlnLysLysValIlePheCysSerArg	420
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RESULT 14

AF403770	AF403770	3433 bp	mRNA	linear	PRI 26-AUG-2001
LOCUS	Macaca fascicularis	lipoprotein lipase precursor, mRNA, complete cds			
DEFINITION					

ACCESSION AF403770

VERSION

KEYWORDS
SOURCE
ORGANISM

Macaca fascicularis (crab-eating macaque)
Macaca fascicularis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecoidea; Macaca.

REFERENCE

AUTHORS	Zhou, J., Wilson, K.M. and Medh, J.D.
TITLE	Identification of novel peroxisome proliferator activated receptor- γ splice variants and induction of PPAR- γ expression by a high-fat diet in monkey macrophages
JOURNAL	Unpublished

JOURNAL

2 (bases 1 to 3433)
Zhou, J., Wilson, K.M. and Medh, J.D.
Direct Submission
Submitted (26-JUL-2001) Internal Medicine, The University of Iowa,
200 Hawkins Drive, Iowa City, IA 52242, USA

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US-10-019-341-3 (1-448) x AF403770 (1-3433)

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 163 GluTyrAlaGluAlaProSerArgLeuSerProAspAspAlaAspPheValAspValLeu 182
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 651 CACACATTCACAGAGGTTCCTTGGCCGAGCATTTGAATCCAGAAACCAAGTTGGGCAT 710
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 771 CGCGTGTATGCAGAGAGAGGCTTGGAGATGTGGACCAAGTATGTAAGTGTCTCCACGAG 830
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891 AGGTGCAGTCCCAAGGAAGCCCTTTGAGAAAGGGCTCTGCTTGTAGTGTAGAAAGACCGC 950
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RESULT 15

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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 3544)
 REFERENCE Nelson,R.M., Marnellos,G., Kammerer,S., Hoyal,C.R., Shi,M.M.,
 Cantor,C.R. and Braun,A.
 Large-Scale Validation of Single Nucleotide Polymorphisms in Gene
 Regions
 JOURNAL Genome Res. (2004) In press
 COMMENT Contact: Andreas Braun
 Pharmaceuticals division
 Sequenom, Inc.
 3595 John Hopkins Court, San Diego, CA 92121, USA
 Tel: 18582029018
 Fax: 18582029020
 Email: abraun@sequenom.com
 Primer A: No primer sequence submitted
 Primer B: No primer sequence submitted
 STS size: 3544.

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Job time : 6096 secs

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